

L Number	Hits	Search Text	DB	Time stamp
5	31	schmitz-gerd.in.	USPAT; US-PGPUB; EPO; JPO; DERWENT	2003/09/10 14:12
6	0	klucken-jochen.in.	USPAT; US-PGPUB; EPO; JPO; DERWENT	2003/09/10 14:12
7	475	atp same binding same cassette	USPAT; US-PGPUB; EPO; JPO; DERWENT	2003/09/10 14:13
8	267	atp same binding same cassette same gene	USPAT; US-PGPUB; EPO; JPO; DERWENT	2003/09/10 14:24
9	59	abca1	USPAT; US-PGPUB; EPO; JPO; DERWENT	2003/09/10 14:24

Sequence Comparison A

RESULT 2

ABCI_MOUSE

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ID   ABC1_MOUSE      STANDARD;          PRT;   2261 AA.
AC   P41233;
DT   01-FEB-1995 (Rel. 31, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   ATP-binding cassette, sub-family A, member 1 (ATP-binding cassette
DE   transporter 1) (ATP-binding cassette 1) (ABC-1).
GN   ABCA1 OR ABC1.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=DBA/2; TISSUE=Macrophage;
RX   MEDLINE=94375008; PubMed=8088782;
RA   Luciani M.F., Denizot F., Savary S., Mattei M.-G., Chimini G.;
RT   "Cloning of two novel ABC transporters mapping on human chromosome
RT   9.";
RL   Genomics 21:150-159(1994).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J;
RX   MEDLINE=21251004; PubMed=11352567;
RA   Qiu Y., Cavellier L., Chiu S., Yang X., Rubin E., Cheng J.-F.;
RT   "Human and mouse ABCA1 comparative sequencing and transgenesis
RT   studies revealing novel regulatory sequences.";
RL   Genomics 73:66-76(2001).
CC   -!- FUNCTION: CAMP-DEPENDENT AND SULFONYLUREA-SENSITIVE ANION
CC   TRANSPORTER. KEY GATEKEEPER INFLUENCING INTRACELLULAR CHOLESTEROL
CC   TRANSPORT (BY SIMILARITY).
CC   -!- TISSUE SPECIFICITY: WIDELY EXPRESSED IN ADULT TISSUES. HIGHEST
CC   LEVELS ARE FOUND IN PREGNANT UTERUS AND UTERUS.
CC   -!- DOMAIN: MULTIFUNCTIONAL POLYPEPTIDE WITH TWO HOMOLOGOUS HALVES,
CC   EACH CONTAINING AN HYDROPHOBIC MEMBRANE-ANCHORING DOMAIN AND AN
CC   ATP BINDING CASSETTE (ABC) DOMAIN.
CC   -!- PTM: Phosphorylation on Ser-2054 regulates phospholipid efflux (By
CC   similarity).
CC   -!- SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY. ABCA SUBFAMILY.
CC   -----
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC   or send an email to license@isb-sib.ch).
CC   -----
DR   EMBL; X75926; CAA53530.1; ALT_INIT.
DR   EMBL; AF287263; AAG39073.1; ALT_INIT.
DR   MGD; MGI:99607; Abcal.
DR   GO; GO:0008203; P:cholesterol metabolism; IDA.
DR   GO; GO:0030301; P:cholesterol transport; IDA.
DR   InterPro; IPR003593; AAA_ATPase.
DR   InterPro; IPR003439; ABC_transporter.
DR   Pfam; PF00005; ABC_tran; 2.
DR   ProDom; PD000006; ABC_transporter; 2.
DR   SMART; SM00382; AAA; 2.
DR   PROSITE; PS00211; ABC_TRANSPORTER_1; 1.
DR   PROSITE; PS50893; ABC_TRANSPORTER_2; 2.
KW   ATP-binding; Glycoprotein; Transmembrane; Transport; Phosphorylation.
FT   TRANSMEM      26      42      POTENTIAL.
FT   TRANSMEM      640     656      POTENTIAL.
FT   TRANSMEM      690     706      POTENTIAL.
FT   TRANSMEM      717     733      POTENTIAL.
FT   TRANSMEM      749     765      POTENTIAL.

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FT	TRANSMEM	771	787	POTENTIAL.
FT	TRANSMEM	1041	1057	POTENTIAL.
FT	TRANSMEM	1351	1367	POTENTIAL.
FT	TRANSMEM	1661	1677	POTENTIAL.
FT	TRANSMEM	1708	1724	POTENTIAL.
FT	TRANSMEM	1737	1753	POTENTIAL.
FT	TRANSMEM	1775	1791	POTENTIAL.
FT	TRANSMEM	1854	1870	POTENTIAL.
FT	NP_BIND	933	940	ATP (POTENTIAL).
FT	NP_BIND	1946	1953	ATP (POTENTIAL).
FT	MOD_RES	1042	1042	PHOSPHORYLATION (BY PKA) (MAJOR) (BY SIMILARITY).
FT	MOD_RES	2054	2054	PHOSPHORYLATION (BY PKA) (MAJOR) (BY SIMILARITY).
FT	CARBOHYD	14	14	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	98	98	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	151	151	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	161	161	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	196	196	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	244	244	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	292	292	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	337	337	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	349	349	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	400	400	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	478	478	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	489	489	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	521	521	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	820	820	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	1144	1144	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	1294	1294	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	1453	1453	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	1499	1499	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	1504	1504	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	1637	1637	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	2044	2044	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	2238	2238	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CONFLICT	1567	1568	MISSING (IN REF. 2).
FT	CONFLICT	2024	2024	MISSING (IN REF. 2).
SQ	SEQUENCE	2261	AA; 254011	MW; FAE62B21FD1D09F9 CRC64;

Query Match 95.1%; Score 10906; DB 1; Length 2261;
 Best Local Similarity 94.8%; Pred. No. 0;
 Matches 2087; Conservative 54; Mismatches 60; Indels 0; Gaps 0;

Qy	1	MPSAGTLPWVQGIICNANNPCFRYPPTGEAPGVVGNFNKSIVARLFSDARRLLLYSQKDT	60
Db	61	MPSAGTLPWVQGIICNANNPCFRYPPTGEAPGVVGNFNKSIVSRLFSDAQRLLLYSQKDT	120
Qy	61	SMKDMRKVLRTLQQIKKSSSNLKLQDFLVDNETFSGFLYHNLSLPKSTVDKMLRADVILH	120
Db	121	SIKDMHKVLRMLRQIKHPNSNLKLQDFLVDNETFSGFLQHNLSPRSTVDSLLQXNVGLQ	180
Qy	121	KVFLQGYQLHLTSLCNGSKSEEMIQLGDQEVSELGCLPREKLAAAERVLRNMDILKPIL	180
Db	181	KVFLQGYQLHLASLCNGSKLEEIIQLGDAEVSALCGLPRKKLDAAERVLRNMDILKPVV	240
Qy	181	RTLNSTSPFPSKELAEATKTLHSLGTLAQELFSMRSWSDMRQEVFMFLTNVNSSSSSTQI	240
Db	241	TKLNSTSHLPTQHLEATTVLLDSLGLAQELFSTKSWSMDMRQEVFMFLTNVNSSSSSTQI	300
Qy	241	YQAVSRIVCGHPEGGGLKIKSLNWEYDNNYKALFGGNGTEEDAETFDNSTTPYCNDLMK	300
Db	301	YQAVSRIVCGHPEGGGLKIKSLNWEYDNNYKALFGGNTEEDVDTFDNSTTPYCNDLMK	360
Qy	301	NLESSPLSRIIWKALKPLLVGKILYTPDTPATRQVMAEVNKTQELAVFHDLEGMWEELS	360
Db	361	NLESSPLSRIIWKALKPLLVGKILYTPDTPATRQVMAEVNKTQELAVFHDLEGMWEELS	420
Qy	361	PKIWTFMENSQEMDLVRMLLDSRDNDHFWEQQLDGLDWTQAQDIVAFLAKHPEDVQSSNGS	420
Db	421	PQIWTFMENSQEMDLVRLDLSRGNDQFWEQQLDGLDWTQAQDIMAFLAKNPEDVQSPNGS	480

Qy 421 VYTWREAFNETNQAI RTISRFMECVNLNKLEPIATEVWLINKSMELLDERKFWAGIVFTG 480
 Db 481 VYTWREAFNETNQAIQTISRFMECVNLNKLEPIPTEVRLINKSMELLDERKFWAGIVFTG 540
 Qy 481 ITPGSIELPHHVYKIRMDIDNVERTNKKIDGYWDPGPRADPFEDMRVWGGFAYLQDVV 540
 Db 541 ITPDSVELPHHVYKIRMDIDNVERTNKKIDGYWDPGPRADPFEDMRVWGGFAYLQDVV 600
 Qy 541 EQAIIRVLTGTTEKKTGVYMQMPYPCYVDDIFLRVMSRSMPLFMTLAWIYSVAVIKIGIV 600
 Db 601 EQAIIRVLTGTSEKKTGVYVQMPYPCYVDDIFLRVMSRSMPLFMTLAWIYSVAVIKSIV 660
 Qy 601 YEKEARLKETMRIMGLDNSILWFSWFISSLIPLLVSAGLLVILKLGNNLLPYSDPSVVFV 660
 Db 661 YEKEARLKETMRIMGLDNGILWFSWVFSSLIPLLVSAGLLVILKLGNNLLPYSDPSVVFV 720
 Qy 661 FLSVFAVVTILQCFLISTLFSRANLAAACGGIYFTLYLPYVLCVAWQDYVGFTLKIFAS 720
 Db 721 FLSVFAVVTILQCFLISTLFSRANLAAACGGIYFTLYLPYVLCVAWQDYVGFSIKIFAS 780
 Qy 721 LLSPVAFGFGCEYFALFEEQIGIGVQWDLNLFESPVVEEDGFNLTTSVSMMLFDTFLYGVMTW 780
 Db 781 LLSPVAFGFGCEYFALFEEQIGIGVQWDLNLFESPVVEEDGFNLTTAVSMMLFDTFLYGVMTW 840
 Qy 781 YIEAVFPGQYGI PRPWYFPCTKSYWFGESDEKSHPGSNQKRISEICMEEEPHKLKLGVS 840
 Db 841 YIEAVFPGQYGI PRPWYFPCTKSYWFGEEIDEKSHPGSSQKGVSEICMEEEPHKLRLGVS 900
 Qy 841 IQNLVKVYRDGMKVAVDGLALNFYEGQITSFLGHNGAGKTTTMSILTGLFPPTSGTAYIL 900
 Db 901 IQNLVKVYRDGMKVAVDGLALNFYEGQITSFLGHNGAGKTTTMSILTGLFPPTSGTAYIL 960
 Qy 901 GKDIRSEMSTIRQNLGVCPOHNVLFDMLTVEEHIWFYARLKLSEKHVKAEMEQLMADV 960
 Db 961 GKDIRSEMSSIRQNLGVCPOHNVLFDMLTVEEHIWFYARLKLSEKHVKAEMEQLMADV 1020
 Qy 961 LPPSKLKSKTSQLSGGMQRKLSVALAFVGGSKVVILDEPTAGVDPYSRRGIWELLLKYRQ 1020
 Db 1021 LPPSKLKSKTSQLSGGMQRKLSVALAFVGGSKVVILDEPTAGVDPYSRRGIWELLLKYRQ 1080
 Qy 1021 GRTIILSTHHMDEADVLGDRIAIISHGKLCCVGSSFLKNQLGTGYLTLVKKDVESLS 1080
 Db 1081 GRTIILSTHHMDEADILGDRIAIISHGKLCCVGSSFLKNQLGTGYLTLVKKDVESLS 1140
 Qy 1081 SCRNSSTVSYLKKEDSVSQSSSDAGLSDHESDTLTIDVSAISNLIRKHVSEARLVEDI 1140
 Db 1141 SCRNSSTVSCLKKEDSVSQSSSDAGLSDHESDTLTIDVSAISNLIRKHVSEARLVEDI 1200
 Qy 1141 GHELTYVLPYEAAKEGAFVELFHEIDRLSDLGISSYGISETTLEEIFLKVAEESGVDAE 1200
 Db 1201 GHELTYVLPYEAAKEGAFVELFHEIDRLSDLGISSYGISETTLEEIFLKVAEESGVDAE 1260
 Qy 1201 TSDGTLPARNRRAFGDKQSCLRPFTEDDAADPNDSIDPESRETDLGMDGKGSYQVK 1260
 Db 1261 TSDGTLPARNRRAFGDKQSCLHPFTEDDAADPNDSIDPESRETDLGMDGKGSYQLK 1320
 Qy 1261 GWKLTQQQFVALLWKRLLIARRSRKGFFAQIVLPAVFVCIALVFSLIVPPFGKYPSLELQ 1320
 Db 1321 GWKLTQQQFVALLWKRLLIARRSRKGFFAQIVLPAVFVCIALVFSLIVPPFGKYPSLELQ 1380
 Qy 1321 PWMYNEQYTFVSNDAPEDTGTLELLNALTDPGFGTRCMEGNPIPDTPCQAGEEWTAP 1380
 Db 1381 PWMYNEQYTFVSNDAPEDMGTQELLNALTDPGFGTRCMEGNPIPDTPCLAGEEDWTISP 1440
 Qy 1381 VPQTIMDLFQNGNWTMKNPSPACQCSSDKIKKMLPVCPPGAGGLPPPQRKQNTADILQDL 1440
 Db 1441 VPQSIVDLFQNGNWTMKNPSPACQCSSDKIKKMLPVCPPGAGGLPPPQRKQNTADILQNL 1500
 Qy 1441 TGRNISDYLVKTYVQIIAKSLKNKIWNENFRYGGFSLGVSNTQALPPSQEVNDATKQMKK 1500

Db 1501 TGRNISDYLVKTYVQIIAKSLKNKIWNNEFRYGGFSLGVSNSQALPPSHEVNDAIKQMKK 1560
 Qy 1501 HLKLAkdSSADrFLNSlGRfMTGLDTRnnVKVfNnKGWHAiSSfLNvINNAILRANLQK 1560
 Db 1561 LLKLTkDTSADrFLSSlGRfMAGLDtKNNVKVfNnKGWHAiSSfLNvINNAILRANLQK 1620
 Qy 1561 GENPSHYGITAFNHPLNLTKQQLSEVAPMTTSVDVLVSICVIFAMSFVPASFVVFLIQR 1620
 Db 1621 GENPSQYGITAFNHPLNLTKQQLSEVALMTTSVDVLVSICVIFAMSFVPASFVVFLIQR 1680
 Qy 1621 VSKAKHLQFISGVKPVYWLNSFVWDMCNYVVPATLVIIIFICFQKSYVSSTNLPVLAL 1680
 Db 1681 VSKAKHLQFISGVKPVYWLNSFVWDMCNYVVPATLVIIIFICFQKSYVSSTNLPVLAL 1740
 Qy 1681 LLLLYGWSITPLMYPASFVFKIPSTAYVVLTSVNLFIGINGSVATFVLELFTDNKLNIN 1740
 Db 1741 LLLLYGWSITPLMYPASFVFKIPSTAYVVLTSVNLFIGINGSVATFVLELFTNNKLNDIN 1800
 Qy 1741 DILKSVFLIFPHFCLGRGLIDMVKNQAMADALERFGENRFVSPLSWDLVGRNLFAMAVEG 1800
 Db 1801 DILKSVFLIFPHFCLGRGLIDMVKNQAMADALERFGENRFVSPLSWDLVGRNLFAMAVEG 1860
 Qy 1801 VVFFLITVLIQYRFFIRPRPVNAKLSPLNDEDEDVRRERQRILDGGGQNDILEIKELTKI 1860
 Db 1861 VVFFLITVLIQYRFFIRPRPVNAKLPPLNDEDEDVRRERQRILDGGGQNDILEIKELTKI 1920
 Qy 1861 YRRKRKPAVDRCVGI PPGE CFLLGVNGAGKSSTFKMLTGDTTVTRGDAFLNRNSILSN 1920
 Db 1921 YRRKRKPAVDRCIGI PPGE CFLLGVNGAGKSTTFKMLTGDTVPVTRGDAFLNKNSILSN 1980
 Qy 1921 IHEVHQNMGYCPQFDAITELLTGREHVEFFALLRGVPEKEVGKVGWAIKLGVLVYGEK 1980
 Db 1981 IHEVHQNMGYCPQFDAITELLTGREHVEFFALLRGVPEKEVGKVGWAIKLGVLVYGEK 2040
 Qy 1981 YAGNYSGGNKRKLSTAMALIGPPVVFLDEPTTGMDPKARRFLWNCALSVVKEGRSVVLT 2040
 Db 2041 YAGNYSGGNKRKLSTAMALIGPPVVFLDEPTTGMDPKARRFLWNCALSVVKEGRSVVLT 2100
 Qy 2041 SHSMEECEALCTRMAIMVNGRFRCLGSVQHLKNRFGDGYTIVVRIAGSNPDLKPVDFFG 2100
 Db 2101 SHSMEECEALCTRMAIMVNGRFRCLGSVQHLKNRFGDGYTIVVRIAGSNPDLKPVDFFG 2160
 Qy 2101 LAFPGSVPEKEHRNMLQYQLPSSLSSLARIFSILSQSKRLHIEDYSVSQTTLDQVFNF 2160
 Db 2161 LAFPGSVLKEKHRNMLQYQLPSSLSSLARIFSILSQSKRLHIEDYSVSQTTLDQVFNF 2220
 Qy 2161 AKDQSDDDHLKDLSLHKNQTVVDVAVLTSFLQDEKVKESYV 2201
 Db 2221 AKDQSDDDHLKDLSLHKNQTVVDVAVLTSFLQDEKVKESYV 2261

Sequence Comparison B

RESULT 1

ABCI_HUMAN

ID ABC1_HUMAN STANDARD; PRT; 2261 AA.
AC O95477; Q96S56; Q96T85; Q9NQV4; Q9UN06; Q9UN07; Q9UN08; Q9UN09;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE ATP-binding cassette, sub-family A, member 1 (ATP-binding cassette
DE transporter 1) (ATP-binding cassette 1) (ABC-1) (Cholesterol efflux
DE regulatory protein).
GN ABCA1 OR ABC1 OR CERP.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20345099; PubMed=10884428;
RA Santamarina-Fojo S., Peterson K.M., Knapper C.L., Qiu Y.,
RA Freeman L.A., Cheng J.-F., Osorio J., Remaley A.T., Yang X.-P.,
RA Haudenschild C.C., Prades C., Chimini G., Blackmon E.E.,
RA Francois T.L., Duverger N., Rubin E.M., Rosier M., Deneffe P.,
RA Fredrickson D.S., Brewer H.B. Jr.;
RT "Complete genomic sequence of the human ABCA1 gene: analysis of the
RT human and mouse ATP-binding cassette A promoter.";
RL Proc. Natl. Acad. Sci. U.S.A. 97:7987-7992(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Skin;
RA Schwartz K., Lawn R.M., Wade D.P.;
RT "ABCA1 gene expression and apoA-I-mediated cholesterol efflux are
RT regulated by LXR.";
RL Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=21251004; PubMed=11352567;
RA Qiu Y., Cavellier L., Chiu S., Yang X., Rubin E., Cheng J.-F.;
RT "Human and mouse ABCA1 comparative sequencing and transgenesis
RT studies revealing novel regulatory sequences.";
RL Genomics 73:66-76(2001).
RN [4]
RP SEQUENCE FROM N.A.
RA Tanaka A.R., Abe-Dohmae S., Arakawa R., Sadanami K., Kidera A.,
RA Kioka N., Amachi T., Yokoyama S., Ueda K.;
RT "A new topological model of functional human ABCA1-signal peptide
RT cleavage and glycosylation of a large extracellular domain.";
RL Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
RN [5]
RP SEQUENCE OF 21-2261 FROM N.A.
RX MEDLINE=99194549; PubMed=10092505;
RA Langmann T., Klucken J., Reil M., Liebisch G., Luciani M.F.,
RA Chimini G., Kaminski W.E., Schmitz G.;
RT "Molecular cloning of the human ATP-binding cassette transporter 1
RT (hABCA1): evidence for sterol-dependent regulation in macrophages.";
RL Biochem. Biophys. Res. Commun. 257:29-33(1999).
RN [6]
RP SEQUENCE OF 21-2261 FROM N.A.
RX MEDLINE=99364413; PubMed=10431238;
RA Rust S., Rosier M., Funke H., Real J., Amoura Z., Piette J.-C.,
RA Deleuze J.-F., Brewer H.B., Duverger N., Deneffe P., Assmann G.;
RT "Tangier disease is caused by mutations in the gene encoding
RT ATP-binding cassette transporter 1.";
RL Nat. Genet. 22:352-355(1999).
RN [7]
RP PHOSPHORYLATION OF SER-1042 AND SER-2054.
RX MEDLINE=22289331; PubMed=12196520;
RA See R.H., Caday-Malcolm R.A., Singaraja R.R., Zhou S., Silverston A.,
RA Huber M.T., Moran J., James E.R., Janoo R., Savill J.M., Rigot V.,

RA Zhang L.H., Wang M., Chimini G., Wellington C.L., Tafuri S.R.,
 RA Hayden M.R.;
 RT "Protein kinase A site-specific phosphorylation regulates ATP-binding
 RT cassette A1 (ABCA1)-mediated phospholipid efflux.";
 RL J. Biol. Chem. 277:41835-41842(2002).
 RN [8]
 RP VARIANTS HDLD2 THR-1091 AND 1893-GLU-ASP-1894 DEL.
 RX MEDLINE=20001430; PubMed=10533863;
 RA Marcil M., Brooks-Wilson A., Clee S.M., Roomp K., Zhang L.-H., Yu L.,
 RA Collins J.A., van Dam M., Molhuizen H.O.F., Loubser O.,
 RA Ouelette B.F.F., Sensen C.W., Fichter K., Mott S., Denis M.,
 RA Boucher B., Pimstone S., Genest J. Jr., Kastelein J.J.P., Hayden M.R.;
 RT "Mutations in the ABC1 gene in familial HDL deficiency with defective
 RT cholesterol efflux.";
 RL Lancet 354:1341-1346(1999).
 RN [9]
 RP VARIANTS HDLD1 ARG-597 AND ARG-1477, AND VARIANT HDLD2 LEU-693 DEL.
 RX MEDLINE=99364411; PubMed=10431236;
 RA Brooks-Wilson A., Marcil M., Clee S.M., Zhang L.-H., Roomp K.,
 RA van Dam M., Yu L., Brewer C., Collins J.A., Molhuizen H.O.F.,
 RA Loubser O., Ouelette B.F.F., Fichter K., Ashbourne-Excoffon K.J.D.,
 RA Sensen C.W., Scherer S., Mott S., Denis M., Martindale D.,
 RA Frohlich J., Morgan K., Koop B., Pimstone S., Kastelein J.J.P.,
 RA Hayden M.R.;
 RT "Mutations in ABC1 in Tangier disease and familial high-density
 RT lipoprotein deficiency.";
 RL Nat. Genet. 22:336-345(1999).
 RN [10]
 RP VARIANTS HDLD1 SER-590; SER-935 AND VAL-937, AND VARIANTS ALA-399 AND
 RP MET-883.
 RX MEDLINE=99364412; PubMed=10431237;
 RA Bodzioch M., Orso E., Klucken J., Langmann T., Boettcher A.,
 RA Diederich W., Drobnik W., Barlage S., Buechler C.,
 RA Porsch-Oezcueromez M., Kaminski W.E., Hahmann H.W., Oette K.,
 RA Rothe G., Aslanidis C., Lackner K.J., Schmitz G.;
 RT "The gene encoding ATP-binding cassette transporter 1 is mutated in
 RT Tangier disease.";
 RL Nat. Genet. 22:347-351(1999).
 RN [11]
 RP VARIANTS HDLD1 ILE-929; ARG-597 AND ARG-1477, AND VARIANTS HDLD2
 RP LEU-693 DEL; THR-1091; 1893-GLU-ASP-1894 DEL AND LEU-2150.
 RX MEDLINE=20540002; PubMed=11086027;
 RA Clee S.M., Kastelein J.J.P., van Dam M., Marcil M., Roomp K.,
 RA Zwarts K.Y., Collins J.A., Roelants R., Tamasawa N., Stulc T.,
 RA Suda T., Ceska R., Boucher B., Rondeau C., DeSouich C.,
 RA Brooks-Wilson A., Molhuizen H.O.F., Frohlich J., Genest J. Jr.,
 RA Hayden M.R.;
 RT "Age and residual cholesterol efflux affect HDL cholesterol levels and
 RT coronary artery disease in ABCA1 heterozygotes.";
 RL J. Clin. Invest. 106:1263-1270(2000).
 RN [12]
 RP VARIANTS HDLD1 ASN-1289 AND HIS-1800.
 RX MEDLINE=20171564; PubMed=10706591;
 RA Brousseau M.E., Schaefer E.J., Dupuis J., Eustace B.,
 RA Van Eerdewegh P., Goldkamp A.L., Thurston L.M., FitzGerald M.G.,
 RA Yasek-McKenna D., O'Neill G., Eberhart G.P., Weiffenbach B.,
 RA Ordovas J.M., Freeman M.W., Brown R.H. Jr., Gu J.Z.;
 RT "Novel mutations in the gene encoding ATP-binding cassette 1 in four
 RT tangier disease kindreds.";
 RL J. Lipid Res. 41:433-441(2000).
 RN [13]
 RP VARIANT HDLD1 ASP-1046, VARIANT HDLD2 CYS-230, AND VARIANTS LYS-219;
 RP ILE-825; MET-883 AND LYS-1587.
 RX MEDLINE=20396633; PubMed=10938021;
 RA Wang J., Burnett J.R., Near S., Young K., Zinman B., Hanley A.J.G.,
 RA Connelly P.W., Harris S.B., Hegele R.A.;
 RT "Common and rare ABCA1 variants affecting plasma HDL cholesterol.";
 RL Arterioscler. Thromb. Vasc. Biol. 20:1983-1989(2000).
 RN [14]
 RP VARIANT HDLD1 TRP-587, AND VARIANT LEU-2168.
 RX MEDLINE=21157002; PubMed=11257260;

RA Bertolini S., Pisciotto L., Seri M., Cusano R., Cantafora A.,
 RA Calabresi L., Franceschini G., Ravazzolo R., Calandra S.;
 RT "A point mutation in ABC1 gene in a patient with severe premature
 RT coronary heart disease and mild clinical phenotype of Tangier
 RT disease.";
 RL Atherosclerosis 154:599-605(2001).
 RN [15]
 RP VARIANTS LYS-219; MET-883 AND ASP-1172.
 RX MEDLINE=21157003; PubMed=11257261;
 RA Brousseau M.E., Bodzioch M., Schaefer E.J., Goldkamp A.L., Kielar D.,
 RA Probst M., Ordovas J.M., Aslanidis C., Lackner K.J.,
 RA Bloomfield Rubins H., Collins D., Robins S.J., Wilson P.W.F.,
 RA Schmitz G.;
 RT "Common variants in the gene encoding ATP-binding cassette transporter
 RT 1 in men with low HDL cholesterol levels and coronary heart disease.";
 RL Atherosclerosis 154:607-611(2001).
 RN [16]
 RP VARIANT HDLD1 LEU-1506.
 RX MEDLINE=21369429; PubMed=11476961;
 RA Lapicka-Bodzioch K., Bodzioch M., Kruell M., Kielar D., Probst M.,
 RA Kiec B., Andrikovics H., Boettcher A., Hubacek J., Aslanidis C.,
 RA Suttorp N., Schmitz G.;
 RT "Homogeneous assay based on 52 primer sets to scan for mutations of
 RT the ABCA1 gene and its application in genetic analysis of a new
 RT patient with familial high-density lipoprotein deficiency syndrome.";
 RL Biochim. Biophys. Acta 1537:42-48(2001).
 RN [17]
 RP VARIANTS HDLD1 ASN-1289 AND TRP-2081, AND VARIANT LYS-219.
 RX MEDLINE=21369433; PubMed=11476965;
 RA Huang W., Moriyama K., Koga T., Hua H., Ageta M., Kawabata S.,
 RA Mawatari K., Imamura T., Eto T., Kawamura M., Teramoto T., Sasaki J.;
 RT "Novel mutations in ABCA1 gene in Japanese patients with Tangier
 RT disease and familial high density lipoprotein deficiency with
 RT coronary heart disease.";
 RL Biochim. Biophys. Acta 1537:71-78(2001).
 RN [18]
 RP VARIANTS LYS-219; ALA-399; MET-771; PRO-774; ASN-776; ILE-825;
 RP MET-883; ASP-1172; LYS-1587 AND CYS-1731.
 RX MEDLINE=21138379; PubMed=11238261;
 RA Clee S.M., Zwiderman A.H., Engert J.C., Zwarts K.Y.,
 RA Molhuizen H.O.F., Roomp K., Jukema J.W., van Wijland M., van Dam M.,
 RA Hudson T.J., Brooks-Wilson A., Genest J. Jr., Kastelein J.J.P.,
 RA Hayden M.R.;
 RT "Common genetic variation in ABCA1 is associated with altered
 RT lipoprotein levels and a modified risk for coronary artery disease.";
 RL Circulation 103:1198-1205(2001).
 RN [19]
 RP VARIANT HDLD1 THR-255, AND VARIANT ATHEROSCLEROSIS ASP-1611.
 RX MEDLINE=21645894; PubMed=11785958;
 RA Nishida Y., Hirano K., Tsukamoto K., Nagano M., Ikegami C., Roomp K.,
 RA Ishihara M., Sakane N., Zhang Z., Tsujii K., Matsuyama A., Ohama T.,
 RA Matsuura F., Ishigami M., Sakai N., Hiraoka H., Hattori H.,
 RA Wellington C., Yoshida Y., Misugi S., Hayden M.R., Egashira T.,
 RA Yamashita S., Matsuzawa Y.;
 RT "Expression and functional analyses of novel mutations of ATP-binding
 RT cassette transporter-1 in Japanese patients with high-density
 RT lipoprotein deficiency.";
 RL Biochem. Biophys. Res. Commun. 290:713-721(2002).
 CC -!- FUNCTION: cAMP-dependent and sulfonylurea-sensitive anion
 CC transporter. Key gatekeeper influencing intracellular cholesterol
 CC transport.
 CC -!- TISSUE SPECIFICITY: Widely expressed, but most abundant in
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Query Match 100.0%; Score 11466; DB 1; Length 2261;
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Db	901	IQNLVKVYRDGMKVAVDGLALNFYEGQITSFLGHNGAGKTTTMSILTGLFPPTSGTAYIL	960
Qy	901	GKDIRSEMSTIRQNLGVCPQHNVLFDMLTVEEHIWIFYARLKGKSEKHVKAEMEQMALDVG	960
Db	961	GKDIRSEMSTIRQNLGVCPQHNVLFDMLTVEEHIWIFYARLKGKSEKHVKAEMEQMALDVG	1020
Qy	961	LPSSKLKSKTSQLSGGMQRKLSVALAFVGGSKVVILDEPTAGVDPYSRRGIWELLLKYRQ	1020
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09786635 Results

SEQ ID NO: 1

SUMMARIES

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AF165281

LOCUS AF165281 9497 bp mRNA linear PRI 17-AUG-1999

DEFINITION Homo sapiens ATP cassette binding transporter 1 (ABC1) mRNA, complete cds.

ACCESSION AF165281

VERSION AF165281.1 GI:5734100

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 9497)

AUTHORS Rust, S., Rosier, M., Funke, H., Real, J., Amoura, Z., Piette, J.C., Deleuze, J.F., Brewer, H.B., Duverger, N., Deneffe, P. and Assmann, G.

TITLE Tangier disease is caused by mutations in the gene encoding

ATP-binding cassette transporter 1

JOURNAL Nat. Genet. 22 (4), 352-355 (1999)

MEDLINE 99364413

PUBMED 10431238

REFERENCE 2 (bases 1 to 9497)

AUTHORS Rust, S., Rosier, M., Funke, H., Real, J., Amoura, Z., Piette, J.C., Deleuze, J.F., Brewer, H.B., Duverger, N., Deneffe, P. and Assmann, G.

TITLE Direct Submission

JOURNAL Submitted (01-JUL-1999) Genomics, Rhone-Poulenc Rorer, 2 rue Gaston Cr#mieux, Evry 91006, France

FEATURES Location/Qualifiers

source

1..9497

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gene
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Db	601		AAACTGGCTGCAGCAGAGCGAGTACTTCGTTCCAACATGGACATCCTGAAGCCAATCCTG	660
Qy	661		AGAACACTAAACTCTACATCTCCCTTCCCGAGCAAGGAGCTGGCCGAAGCCACAAAAACA	720
Db	661		AGAACACTAAACTCTACATCTCCCTTCCCGAGCAAGGAGCTGGCCGAAGCCACAAAAACA	720
Qy	721		TTGCTGCATAGTCTTGGGACTCTGGCCAGGAGCTGTTGAGCATGAGAAGCTGGAGTGAC	780
Db	721		TTGCTGCATAGTCTTGGGACTCTGGCCAGGAGCTGTTGAGCATGAGAAGCTGGAGTGAC	780
Qy	781		ATGCGACAGGAGGTGATGTTTCTGACCAATGTGAACAGCTCCAGCTCCTCCACCCAAATC	840
Db	781		ATGCGACAGGAGGTGATGTTTCTGACCAATGTGAACAGCTCCAGCTCCTCCACCCAAATC	840
Qy	841		TACCAGGCTGTGTCTCGTATTGTCTGCGGGCATCCCGAGGGAGGGGGGCTGAAGATCAAG	900
Db	841		TACCAGGCTGTGTCTCGTATTGTCTGCGGGCATCCCGAGGGAGGGGGGCTGAAGATCAAG	900
Qy	901		TCTCTCAACTGGTATGAGGACAACAACCTACAAGCCCTCTTTGGAGGCAATGGCACTGAG	960
Db	901		TCTCTCAACTGGTATGAGGACAACAACCTACAAGCCCTCTTTGGAGGCAATGGCACTGAG	960
Qy	961		GAAGATGCTGAAACCTTCTATGACAACCTCTACAACCTCTTACTGCAATGATTTGATGAAG	1020
Db	961		GAAGATGCTGAAACCTTCTATGACAACCTCTACAACCTCTTACTGCAATGATTTGATGAAG	1020
Qy	1021		AATTTGGAGTCTAGTCTCTTTTCCCGCATTATCTGGAAAGCTCTGAAGCCGCTGCTCGTT	1080
Db	1021		AATTTGGAGTCTAGTCTCTTTTCCCGCATTATCTGGAAAGCTCTGAAGCCGCTGCTCGTT	1080
Qy	1081		GGGAAGATCCTGTATACACCTGACACTCCAGCCACAAGGCAGGTCATGGCTGAGGTGAAC	1140
Db	1081		GGGAAGATCCTGTATACACCTGACACTCCAGCCACAAGGCAGGTCATGGCTGAGGTGAAC	1140
Qy	1141		AAGACCTTCCAGGAACCTGGCTGTGTTCCATGATCTGGAAGGCATGTGGGAGGAACTCAGC	1200
Db	1141		AAGACCTTCCAGGAACCTGGCTGTGTTCCATGATCTGGAAGGCATGTGGGAGGAACTCAGC	1200
Qy	1201		CCCAAGATCTGGACCTTCATGGAGAACAGCCAAGAAATGGACCTTGTCCGGATGCTGTTG	1260
Db	1201		CCCAAGATCTGGACCTTCATGGAGAACAGCCAAGAAATGGACCTTGTCCGGATGCTGTTG	1260

Qy	1261	GACAGCAGGGACAATGACCAC	TTTTGGGAACAGCAGTTGGATGGCTTAGATTGGACAGCC	1320
Db	1261	GACAGCAGGGACAATGACCAC	TTTTGGGAACAGCAGTTGGATGGCTTAGATTGGACAGCC	1320
Qy	1321	CAAGACATCGTGGCGTTTTTGGCCAAGCACCAGAGGATGTCCAGTCCAGTAATGGTTCT	1380	
Db	1321	CAAGACATCGTGGCGTTTTTGGCCAAGCACCAGAGGATGTCCAGTCCAGTAATGGTTCT	1380	
Qy	1381	GTGTACACCTGGAGAGAAGCTTTCAACGAGACTAACCAGGCAATCCGGACCATATCTCGC	1440	
Db	1381	GTGTACACCTGGAGAGAAGCTTTCAACGAGACTAACCAGGCAATCCGGACCATATCTCGC	1440	
Qy	1441	TTTCATGGAGTGTGTCAACCTGAACAAGCTAGAACCATAGCAACAGAAGTCTGGCTCATC	1500	
Db	1441	TTTCATGGAGTGTGTCAACCTGAACAAGCTAGAACCATAGCAACAGAAGTCTGGCTCATC	1500	
Qy	1501	AACAAGTCCATGGAGCTGCTGGATGAGAGGAAGTTCTGGGCTGGTATTGTGTTCAC	1560	
Db	1501	AACAAGTCCATGGAGCTGCTGGATGAGAGGAAGTTCTGGGCTGGTATTGTGTTCAC	1560	
Qy	1561	ATTACTCCAGGCAGCATTGAGCTGCCCCATCATGTCAAGTACAAGATCCGAATGGACATT	1620	
Db	1561	ATTACTCCAGGCAGCATTGAGCTGCCCCATCATGTCAAGTACAAGATCCGAATGGACATT	1620	
Qy	1621	GACAAATGTGGAGAGGACAAATAAAATCAAGGATGGGTACTGGGACCCTGGTCTCGAGCT	1680	
Db	1621	GACAAATGTGGAGAGGACAAATAAAATCAAGGATGGGTACTGGGACCCTGGTCTCGAGCT	1680	
Qy	1681	GACCCCTTTGAGGACATGCGGTACGTCTGGGGGGGCTTCGCCTACTTGCAGGATGTGGTG	1740	
Db	1681	GACCCCTTTGAGGACATGCGGTACGTCTGGGGGGGCTTCGCCTACTTGCAGGATGTGGTG	1740	
Qy	1741	GAGCAGGCAATCATCAGGGTGTGACGGGCACCGAGAAGAAAACCTGGTGTCTATATGCAA	1800	
Db	1741	GAGCAGGCAATCATCAGGGTGTGACGGGCACCGAGAAGAAAACCTGGTGTCTATATGCAA	1800	
Qy	1801	CAGATGCCCTATCCCTGTTACGTTGATGACATCTTTCTGCGGGTGATGAGCCGGTCAATG	1860	
Db	1801	CAGATGCCCTATCCCTGTTACGTTGATGACATCTTTCTGCGGGTGATGAGCCGGTCAATG	1860	
Qy	1861	CCCCCTCTTCATGACGCTGGCCTGGATTACTCAGTGGCTGTGATCATCAAGGGCATCGTG	1920	
Db	1861	CCCCCTCTTCATGACGCTGGCCTGGATTACTCAGTGGCTGTGATCATCAAGGGCATCGTG	1920	
Qy	1921	TATGAGAAGGAGGCACGGCTGAAAGAGACCATGCGGATCATGGGCCTGGACAACAGCATC	1980	
Db	1921	TATGAGAAGGAGGCACGGCTGAAAGAGACCATGCGGATCATGGGCCTGGACAACAGCATC	1980	
Qy	1981	CTCTGGTTTAGCTGGTTCATTAGTAGCCTATTCTCTTCTTGTGAGCGCTGGCCTGCTA	2040	
Db	1981	CTCTGGTTTAGCTGGTTCATTAGTAGCCTATTCTCTTCTTGTGAGCGCTGGCCTGCTA	2040	
Qy	2041	GTGGTCATCCTGAAGTTAGGAAACCTGCTGCCCTACAGTGATCCCAGCGTGGTGTGTTGTC	2100	
Db	2041	GTGGTCATCCTGAAGTTAGGAAACCTGCTGCCCTACAGTGATCCCAGCGTGGTGTGTTGTC	2100	
Qy	2101	TTCTGTCCGTGTTTGCTGTGGTGACAATCCTGCAGTGCTTCTGATTAGCACACTCTTC	2160	
Db	2101	TTCTGTCCGTGTTTGCTGTGGTGACAATCCTGCAGTGCTTCTGATTAGCACACTCTTC	2160	
Qy	2161	TCCAGAGCCAACCTGGCAGCAGCCTGTGGGGGCATCATCTACTTCACGCTGTACCTGCCC	2220	
Db	2161	TCCAGAGCCAACCTGGCAGCAGCCTGTGGGGGCATCATCTACTTCACGCTGTACCTGCCC	2220	
Qy	2221	TACGTCTGTGTGTGGCATGGCAGGACTACGTGGGCTTCACACTCAAGATCTTCGCTAGC	2280	
Db	2221	TACGTCTGTGTGTGGCATGGCAGGACTACGTGGGCTTCACACTCAAGATCTTCGCTAGC	2280	
Qy	2281	CTGCTGTCTCCTGTGGCTTTTGGGTTTGGCTGTGAGTACTTTGCCCTTTTGGAGGAGCAG	2340	
Db	2281	CTGCTGTCTCCTGTGGCTTTTGGGTTTGGCTGTGAGTACTTTGCCCTTTTGGAGGAGCAG	2340	

Qy	2341	GGCATTGGAGTGAGTGGGACAACTGTTTGAGAGTCCTGTGGAGGAAGATGGCTTCAAT	2400
Db	2341	GGCATTGGAGTGAGTGGGACAACTGTTTGAGAGTCCTGTGGAGGAAGATGGCTTCAAT	2400
Qy	2401	CTCACCACCTTCGGTCTCCATGATGCTGTTTGACACCTTCCTCTATGGGGTGATGACCTGG	2460
Db	2401	CTCACCACCTTCGGTCTCCATGATGCTGTTTGACACCTTCCTCTATGGGGTGATGACCTGG	2460
Qy	2461	TACATTGAGGCTGTCTTTCCAGGCCAGTACGGAATCCCAGGCCCTGGTATTTTCCTTGC	2520
Db	2461	TACATTGAGGCTGTCTTTCCAGGCCAGTACGGAATCCCAGGCCCTGGTATTTTCCTTGC	2520
Qy	2521	ACCAAGTCCTACTGGTTTGGCGAGGAAAGTGATGAGAAGAGCCACCCTGGTTCCAACCAG	2580
Db	2521	ACCAAGTCCTACTGGTTTGGCGAGGAAAGTGATGAGAAGAGCCACCCTGGTTCCAACCAG	2580
Qy	2581	AAGAGAATATCAGAAATCTGCATGGAGGAGGAACCCACCCACTTGAAGCTGGGCGTGTCC	2640
Db	2581	AAGAGAATATCAGAAATCTGCATGGAGGAGGAACCCACCCACTTGAAGCTGGGCGTGTCC	2640
Qy	2641	ATTCAGAACCTGGTAAAAGTCTACCGAGATGGGATGAAGGTGGCTGTCGATGGCCTGGCA	2700
Db	2641	ATTCAGAACCTGGTAAAAGTCTACCGAGATGGGATGAAGGTGGCTGTCGATGGCCTGGCA	2700
Qy	2701	CTGAATTTTATGAGGGCCAGATCACCTCCTTCCTGGGCCACAATGGAGCGGGGAAGACG	2760
Db	2701	CTGAATTTTATGAGGGCCAGATCACCTCCTTCCTGGGCCACAATGGAGCGGGGAAGACG	2760
Qy	2761	ACCACCATGTCAATCCTGACCGGTTGTTCCTCCCGACCTCGGGCACCGCCTACATCCTG	2820
Db	2761	ACCACCATGTCAATCCTGACCGGTTGTTCCTCCCGACCTCGGGCACCGCCTACATCCTG	2820
Qy	2821	GGAAAAGACATTCTGCTCTGAGATGAGCACCATCCGGCAGAACCTGGGGGTCTGTCCCCAG	2880
Db	2821	GGAAAAGACATTCTGCTCTGAGATGAGCACCATCCGGCAGAACCTGGGGGTCTGTCCCCAG	2880
Qy	2881	CATAACGTGCTGTTTGACATGCTGACTGTCTGAAGAACACATCTGGTTCTATGCCCGCTTG	2940
Db	2881	CATAACGTGCTGTTTGACATGCTGACTGTCTGAAGAACACATCTGGTTCTATGCCCGCTTG	2940
Qy	2941	AAAGGGCTCTCTGAGAAGCACGTGAAGGCGGAGATGGAGCAGATGGCCCTGGATGTTGGT	3000
Db	2941	AAAGGGCTCTCTGAGAAGCACGTGAAGGCGGAGATGGAGCAGATGGCCCTGGATGTTGGT	3000
Qy	3001	TTGCCATCAAGCAAGCTGAAAAGCAAAACAAGCCAGCTGTGAGGTGGAATGCAGAGAAAAG	3060
Db	3001	TTGCCATCAAGCAAGCTGAAAAGCAAAACAAGCCAGCTGTGAGGTGGAATGCAGAGAAAAG	3060
Qy	3061	CTATCTGTGGCCTTGGCCTTTGTCTGGGGGATCTAAGGTTGTCTATTCTGGATGAACCCACA	3120
Db	3061	CTATCTGTGGCCTTGGCCTTTGTCTGGGGGATCTAAGGTTGTCTATTCTGGATGAACCCACA	3120
Qy	3121	GCTGGTGTGGACCCTTACTCCCGCAGGGGAATATGGGAGCTGCTGCTGAAATACCGACAA	3180
Db	3121	GCTGGTGTGGACCCTTACTCCCGCAGGGGAATATGGGAGCTGCTGCTGAAATACCGACAA	3180
Qy	3181	GGCCGCACCATATTCTCTCTACACACCACATGGATGAAGCGGACGTCCTGGGGGACAGG	3240
Db	3181	GGCCGCACCATATTCTCTCTACACACCACATGGATGAAGCGGACGTCCTGGGGGACAGG	3240
Qy	3241	ATTGCCATCATCTCCCATGGGAAGCTGTGCTGTGTGGGCTCCTCCCTGTTTCTGAAGAAC	3300
Db	3241	ATTGCCATCATCTCCCATGGGAAGCTGTGCTGTGTGGGCTCCTCCCTGTTTCTGAAGAAC	3300
Qy	3301	CAGCTGGGAACAGGCTACTACCTGACCTTGGTCAAGAAAGATGTGGAATCCTCCCTCAGT	3360
Db	3301	CAGCTGGGAACAGGCTACTACCTGACCTTGGTCAAGAAAGATGTGGAATCCTCCCTCAGT	3360
Qy	3361	TCCTGCAGAAACAGTAGTAGCACTGTGTACATACCTGAAAAAGGAGGACAGTGTTCCTCAG	3420

Db 3361 TCCTGCAGAAACAGTAGTAGCTGTGTACCTGAAAAAGGAGGACAGTGTTCCTCAG 3420
 Qy 3421 AGCAGTTCTGATGCTGGCCTGGGCAGCGACCATGAGAGTGACACGCTGACCATCGATGTC 3480
 |||||
 Db 3421 AGCAGTTCTGATGCTGGCCTGGGCAGCGACCATGAGAGTGACACGCTGACCATCGATGTC 3480
 Qy 3481 TCTGCTATCTCCAACCTCATCAGGAAGCATGTGTCTGAAGCCCGGCTGGTGAAGACATA 3540
 |||||
 Db 3481 TCTGCTATCTCCAACCTCATCAGGAAGCATGTGTCTGAAGCCCGGCTGGTGAAGACATA 3540
 Qy 3541 GGGCATGAGCTGACCTATGTGCTGCCATATGAAGCTGCTAAGGAGGGAGCCTTTGTGGAA 3600
 |||||
 Db 3541 GGGCATGAGCTGACCTATGTGCTGCCATATGAAGCTGCTAAGGAGGGAGCCTTTGTGGAA 3600
 Qy 3601 CTCTTTCATGAGATTGATGACCGGCTCTCAGACCTGGGCATTCTAGTTATGGCATCTCA 3660
 |||||
 Db 3601 CTCTTTCATGAGATTGATGACCGGCTCTCAGACCTGGGCATTCTAGTTATGGCATCTCA 3660
 Qy 3661 GAGACGACCTTGAAGAAATATTCTCAAGGTGGCCGAAGAGAGTGGGGTGGATGCTGAG 3720
 |||||
 Db 3661 GAGACGACCTTGAAGAAATATTCTCAAGGTGGCCGAAGAGAGTGGGGTGGATGCTGAG 3720
 Qy 3721 ACCTCAGATGGTACCTTGCCAGCAAGACGAAACAGGCGGGCCTTCGGGGACAAGCAGAGC 3780
 |||||
 Db 3721 ACCTCAGATGGTACCTTGCCAGCAAGACGAAACAGGCGGGCCTTCGGGGACAAGCAGAGC 3780
 Qy 3781 TGTCTTCGCCCCGTTCACTGAAGATGATGCTGTGATCCAAATGATTCTGACATAGACCCA 3840
 |||||
 Db 3781 TGTCTTCGCCCCGTTCACTGAAGATGATGCTGTGATCCAAATGATTCTGACATAGACCCA 3840
 Qy 3841 GAATCCAGAGAGACAGACTTGCTCAGTGGGATGGATGGCAAAGGGTCTACCAGGTGAAA 3900
 |||||
 Db 3841 GAATCCAGAGAGACAGACTTGCTCAGTGGGATGGATGGCAAAGGGTCTACCAGGTGAAA 3900
 Qy 3901 GGCTGGAACCTTACACAGCAACAGTTTGTGGCCCTTTTGTGGAAGAGACTGCTAATTGCC 3960
 |||||
 Db 3901 GGCTGGAACCTTACACAGCAACAGTTTGTGGCCCTTTTGTGGAAGAGACTGCTAATTGCC 3960
 Qy 3961 AGACGGAGTCGGAAGGATTTTTTGCTCAGATTGTCTTGCCAGCTGTGTTTGTCTGCATT 4020
 |||||
 Db 3961 AGACGGAGTCGGAAGGATTTTTTGCTCAGATTGTCTTGCCAGCTGTGTTTGTCTGCATT 4020
 Qy 4021 GCCCTTGTGTTTCAAGCTGATCGTGCCACCCCTTGGCAAGTACCCAGCCTGGAACCTCAG 4080
 |||||
 Db 4021 GCCCTTGTGTTTCAAGCTGATCGTGCCACCCCTTGGCAAGTACCCAGCCTGGAACCTCAG 4080
 Qy 4081 CCCTGGATGTACAACGAACAGTACACATTTGTGAGCAATGATGCTCCTGAGGACACGGGA 4140
 |||||
 Db 4081 CCCTGGATGTACAACGAACAGTACACATTTGTGAGCAATGATGCTCCTGAGGACACGGGA 4140
 Qy 4141 ACCCTGGAACCTTTAAACGCCCTCACCAAAGACCCTGGCTTCGGGACCCGCTGTATGGAA 4200
 |||||
 Db 4141 ACCCTGGAACCTTTAAACGCCCTCACCAAAGACCCTGGCTTCGGGACCCGCTGTATGGAA 4200
 Qy 4201 GGAAACCAATCCCAGACACGCCCTGCCAGGCAGGGGAGGAAGAGTGGACCACTGCCCCA 4260
 |||||
 Db 4201 GGAAACCAATCCCAGACACGCCCTGCCAGGCAGGGGAGGAAGAGTGGACCACTGCCCCA 4260
 Qy 4261 GTTCCCCAGACCATCATGGACCTCTTCAGAAATGGGAACTGGACAATGCAGAACCCCTTCA 4320
 |||||
 Db 4261 GTTCCCCAGACCATCATGGACCTCTTCAGAAATGGGAACTGGACAATGCAGAACCCCTTCA 4320
 Qy 4321 CCTGCATGCCAGTGTAGCAGCGACAAAATCAAGAAGATGCTGCCTGTGTGTCCCCCAGGG 4380
 |||||
 Db 4321 CCTGCATGCCAGTGTAGCAGCGACAAAATCAAGAAGATGCTGCCTGTGTGTCCCCCAGGG 4380
 Qy 4381 GCAGGGGGGCTGCCTCCTCCACAAAAGAAAACAAAACACTGCAGATATCCTTCAGGACCTG 4440
 |||||
 Db 4381 GCAGGGGGGCTGCCTCCTCCACAAAAGAAAACAAAACACTGCAGATATCCTTCAGGACCTG 4440
 Qy 4441 ACAGGAAGAAACATTTTCGATTATCTGGTGAAGACGTATGTGCAGATCATAGCCAAAAGC 4500

Db	4441	 ACAGGAAGAAACATTTTCGGATTATCTGGTGAAGACGTATGTGCAGATCATAGCCAAAAGC	4500
Qy	4501	TTAAAGAACAAGATCTGGGTGAATGAGTTTAGGTATGGCGGCTTTTCCCTGGGTGTCAGT	4560
Db	4501	TTAAAGAACAAGATCTGGGTGAATGAGTTTAGGTATGGCGGCTTTTCCCTGGGTGTCAGT	4560
Qy	4561	AATACTCAAGCACTTCCTCCGAGTCAAGAAGTTAATGATGCCACCAAACAAATGAAGAAA	4620
Db	4561	AATACTCAAGCACTTCCTCCGAGTCAAGAAGTTAATGATGCCACCAAACAAATGAAGAAA	4620
Qy	4621	CACCTAAAGCTGGCCAAGGACAGTTCTGCAGATCGATTTCTCAACAGCTTGGAAGATTT	4680
Db	4621	CACCTAAAGCTGGCCAAGGACAGTTCTGCAGATCGATTTCTCAACAGCTTGGAAGATTT	4680
Qy	4681	ATGACAGGACTGGACACCAGAAAATAATGTCAAGGTGTGGTTCAATAACAAGGGCTGGCAT	4740
Db	4681	ATGACAGGACTGGACACCAGAAAATAATGTCAAGGTGTGGTTCAATAACAAGGGCTGGCAT	4740
Qy	4741	GCAATCAGCTCTTTCCTGAATGTCATCAACAATGCCATTCTCGGGGCCAACCTGCAAAAG	4800
Db	4741	GCAATCAGCTCTTTCCTGAATGTCATCAACAATGCCATTCTCGGGGCCAACCTGCAAAAG	4800
Qy	4801	GGAGAGAACCCCTAGCCATTATGGAATTACTGCTTTCAATCATCCCCTGAATCTCACCAAG	4860
Db	4801	GGAGAGAACCCCTAGCCATTATGGAATTACTGCTTTCAATCATCCCCTGAATCTCACCAAG	4860
Qy	4861	CAGCAGCTCTCAGAGGTGGCTCCGATGACCACATCAGTGGATGTCCTGTGTCCATCTGT	4920
Db	4861	CAGCAGCTCTCAGAGGTGGCTCCGATGACCACATCAGTGGATGTCCTGTGTCCATCTGT	4920
Qy	4921	GTCATCTTTGCAATGTCCTTCGTCCCAGCCAGCTTTGTCTGATTCTGATCCAGGAGCGG	4980
Db	4921	GTCATCTTTGCAATGTCCTTCGTCCCAGCCAGCTTTGTCTGATTCTGATCCAGGAGCGG	4980
Qy	4981	GTCAGCAAAGCAAAACACCTGCAGTTCATCAGTGGAGTGAAGCCTGTCATCTACTGGCTC	5040
Db	4981	GTCAGCAAAGCAAAACACCTGCAGTTCATCAGTGGAGTGAAGCCTGTCATCTACTGGCTC	5040
Qy	5041	TCTAATTTTGTCTGGGATATGTGCAATTACGTTGTCCCTGCCACACTGGTCATTATCATC	5100
Db	5041	TCTAATTTTGTCTGGGATATGTGCAATTACGTTGTCCCTGCCACACTGGTCATTATCATC	5100
Qy	5101	TTCATCTGCTTCCAGCAGAAGTCCTATGTGTCTCCACCAATCTGCCTGTGCTAGCCCTT	5160
Db	5101	TTCATCTGCTTCCAGCAGAAGTCCTATGTGTCTCCACCAATCTGCCTGTGCTAGCCCTT	5160
Qy	5161	CTACTTTTGTCTGTATGGGTGGTCAATCACACCTCTCATGTACCCAGCCTCCTTTGTGTTC	5220
Db	5161	CTACTTTTGTCTGTATGGGTGGTCAATCACACCTCTCATGTACCCAGCCTCCTTTGTGTTC	5220
Qy	5221	AAGATCCCCAGCACAGCCTATGTGGTGCTACCAGCGTGAACCTCTTCATTGGCATTAAAT	5280
Db	5221	AAGATCCCCAGCACAGCCTATGTGGTGCTACCAGCGTGAACCTCTTCATTGGCATTAAAT	5280
Qy	5281	GGCAGCGTGGCCACCTTTGTGTCTGGAGCTGTTACCGACAATAAGCTGAATAATATCAAT	5340
Db	5281	GGCAGCGTGGCCACCTTTGTGTCTGGAGCTGTTACCGACAATAAGCTGAATAATATCAAT	5340
Qy	5341	GATATCCTGAAGTCCGTGTTCTTGATCTTCCCACATTTTGCCTGGGACGAGGGCTCATC	5400
Db	5341	GATATCCTGAAGTCCGTGTTCTTGATCTTCCCACATTTTGCCTGGGACGAGGGCTCATC	5400
Qy	5401	GACATGGTGAAAAACAGGCAATGGCTGATGCCCTGGAAAGGTTTGGGGAGAATCGCTTT	5460
Db	5401	GACATGGTGAAAAACAGGCAATGGCTGATGCCCTGGAAAGGTTTGGGGAGAATCGCTTT	5460
Qy	5461	GTGTCACCATTATCTTGGGACTTGGTGGGACGAAACCTCTTCGCCATGGCCGTGGAAGGG	5520
Db	5461	GTGTCACCATTATCTTGGGACTTGGTGGGACGAAACCTCTTCGCCATGGCCGTGGAAGGG	5520

Qy	5521	GTGGTGTTCCTCCTCATTACTGTTCTGATCCAGTACAGATTCTTCATCAGGCCAGACCT	5580
Db	5521	GTGGTGTTCCTCCTCATTACTGTTCTGATCCAGTACAGATTCTTCATCAGGCCAGACCT	5580
Qy	5581	GTAATGCAAAGCTATCTCCTCTGAATGATGAAGATGAAGATGTGAGGCGGAAAGACAG	5640
Db	5581	GTAATGCAAAGCTATCTCCTCTGAATGATGAAGATGAAGATGTGAGGCGGAAAGACAG	5640
Qy	5641	AGAATTCTTGATGGTGGAGGCCAGAATGACATCTTAGAAATCAAGGAGTTGACGAAGATA	5700
Db	5641	AGAATTCTTGATGGTGGAGGCCAGAATGACATCTTAGAAATCAAGGAGTTGACGAAGATA	5700
Qy	5701	TATAGAAGGAAGCGGAAGCCTGCTGTTGACAGGATTTGCGTGGGCATTCTCCTGGTGAG	5760
Db	5701	TATAGAAGGAAGCGGAAGCCTGCTGTTGACAGGATTTGCGTGGGCATTCTCCTGGTGAG	5760
Qy	5761	TGCTTTGGGCTCCTGGGAGTTAATGGGGCTGGAAAATCATCAACTTTCAAGATGTTAACA	5820
Db	5761	TGCTTTGGGCTCCTGGGAGTTAATGGGGCTGGAAAATCATCAACTTTCAAGATGTTAACA	5820
Qy	5821	GGAGATACCACTGTTACCAGAGGAGATGCTTTCCTTAACAGAAATAGTATCTTATCAAAC	5880
Db	5821	GGAGATACCACTGTTACCAGAGGAGATGCTTTCCTTAACAGAAATAGTATCTTATCAAAC	5880
Qy	5881	ATCCATGAAGTACATCAGAACATGGGCTACTGCCCTCAGTTTGATGCCATCACAGAGCTG	5940
Db	5881	ATCCATGAAGTACATCAGAACATGGGCTACTGCCCTCAGTTTGATGCCATCACAGAGCTG	5940
Qy	5941	TTGACTGGGAGAGAACACGTGGAGTTCTTTGCCCTTTTGAGAGGAGTCCCAGAGAAAGAA	6000
Db	5941	TTGACTGGGAGAGAACACGTGGAGTTCTTTGCCCTTTTGAGAGGAGTCCCAGAGAAAGAA	6000
Qy	6001	GTTGGCAAGGTTGGTGAGTGGGCGATTTCGGAACCTGGGCCTCGTGAAGTATGGAGAAAA	6060
Db	6001	GTTGGCAAGGTTGGTGAGTGGGCGATTTCGGAACCTGGGCCTCGTGAAGTATGGAGAAAA	6060
Qy	6061	TATGCTGGTAACATATAGTGGAGGCAACAAACGCAAGCTCTCTACAGCCATGGCTTTGATC	6120
Db	6061	TATGCTGGTAACATATAGTGGAGGCAACAAACGCAAGCTCTCTACAGCCATGGCTTTGATC	6120
Qy	6121	GGCGGGCCTCCTGTGGTGTTTCTGGATGAACCCACCACAGGCATGGATCCCAAAGCCCGG	6180
Db	6121	GGCGGGCCTCCTGTGGTGTTTCTGGATGAACCCACCACAGGCATGGATCCCAAAGCCCGG	6180
Qy	6181	CGGTTCTTGTGGAATTGTGCCCTAAGTGTTGTCAAGGAGGGGAGATCAGTAGTGCTTACA	6240
Db	6181	CGGTTCTTGTGGAATTGTGCCCTAAGTGTTGTCAAGGAGGGGAGATCAGTAGTGCTTACA	6240
Qy	6241	TCTCATAGTATGGAAGAATGTGAAGCTCTTTGCACTAGGATGGCAATCATGGTCAATGGA	6300
Db	6241	TCTCATAGTATGGAAGAATGTGAAGCTCTTTGCACTAGGATGGCAATCATGGTCAATGGA	6300
Qy	6301	AGGTTTCAGGTGCCTTGGCAGTGTCCAGCATCTAAAAAATAGGTTTGAGATGGTTATACA	6360
Db	6301	AGGTTTCAGGTGCCTTGGCAGTGTCCAGCATCTAAAAAATAGGTTTGAGATGGTTATACA	6360
Qy	6361	ATAGTTGTACGAATAGCAGGGTCCAACCCGACCTGAAGCCTGTCCAGGATTCTTTGGA	6420
Db	6361	ATAGTTGTACGAATAGCAGGGTCCAACCCGACCTGAAGCCTGTCCAGGATTCTTTGGA	6420
Qy	6421	CTTGCAATTCCTGGAAGTGTTCCAAAAGAGAAACACCGGAACATGCTACAATACCAGCTT	6480
Db	6421	CTTGCAATTCCTGGAAGTGTTCCAAAAGAGAAACACCGGAACATGCTACAATACCAGCTT	6480
Qy	6481	CCATCTTCATTATCTTCTCTGGCCAGGATATTGAGCATCCTCTCCAGAGCAAAAAGCGA	6540
Db	6481	CCATCTTCATTATCTTCTCTGGCCAGGATATTGAGCATCCTCTCCAGAGCAAAAAGCGA	6540
Qy	6541	CTCCACATAGAAGACTACTCTGTTTCTCAGACAACACTTGACCAAGTATTTGTGAACCTT	6600
Db	6541	CTCCACATAGAAGACTACTCTGTTTCTCAGACAACACTTGACCAAGTATTTGTGAACCTT	6600

Qy 6601 GCCAAGGACCAAAAGTGATGATGACCACTTAAAGACCTCTCATTACACAAAAACCAGACA 6660
 |||||
 Db 6601 GCCAAGGACCAAAAGTGATGATGACCACTTAAAGACCTCTCATTACACAAAAACCAGACA 6660
 Qy 6661 GTAGTGGACGTTGCAGTTCTCACATCTTTTCTACAGGATGAGAAAGTGAAAGAAAGCTAT 6720
 |||||
 Db 6661 GTAGTGGACGTTGCAGTTCTCACATCTTTTCTACAGGATGAGAAAGTGAAAGAAAGCTAT 6720
 Qy 6721 GTATGAAGAATCCTGTTTCATACGGGGTGGCTGAAAGTAAAGAGGGACTAGACTTTCCTTT 6780
 |||||
 Db 6721 GTATGAAGAATCCTGTTTCATACGGGGTGGCTGAAAGTAAAGAGGNACTAGACTTTCCTTT 6780
 Qy 6781 GCACCATGTGAAGTGTGTGGAGAAAAGAGCCAGAAGTTGATGTGGGAAGAAGTAAACTG 6840
 |||||
 Db 6781 GCACCATGTGAAGTGTGTGGAGAAAAGAGCCAGAAGTTGATGTGGGAAGAAGTAAACTG 6840
 Qy 6841 GATACTGTACTGATACTATTCAATGCAATGCAATTCAATG 6880
 |||||
 Db 6841 GATACTGTACTGATACTATTCAATGCAATGCAATTCAATG 6880

SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	6880	100.0	6880	21	AAZ94734	Human ATP binding
2	6880	100.0	6880	22	AAI70314	Human ATP binding
3	6880	100.0	7260	22	AAD21326	Human ATP binding
4	6880	100.0	7260	22	AAI70315	Human ATP binding
5	6879	100.0	9497	24	ABV78020	Hypoxia-regulated
6	6876.8	100.0	6880	22	AAD21325	Human ATP binding
7	6875.8	99.9	9741	22	AAS06120	Human ABC1 DNA seq
8	6875.8	99.9	9741	24	AAD37273	Human ABC1 full-le
9	6875.8	99.9	9854	22	AAS06121	Human ABC1 DNA seq
10	6875.8	99.9	9870	24	ABN99301	Polymorphic human
11	6875.8	99.9	9870	24	ABN99302	Polymorphic human
12	6875.8	99.9	9870	24	ABN99303	Polymorphic human
13	6875.8	99.9	9870	24	ABN99324	Polymorphic human
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Polymorphic human

SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	430.8	6.3	5894	3	US-08-665-259-24	Sequence 24, Appl
2	430.8	6.3	5894	3	US-08-762-500-24	Sequence 24, Appl
3	430.8	6.3	6525	3	US-08-762-500-74	Sequence 74, Appl
4	99.4	1.4	1008	4	US-09-252-991A-4266	Sequence 4266, Ap
c 5	98.8	1.4	999	4	US-09-252-991A-4588	Sequence 4588, Ap
6	89.4	1.3	1614	4	US-09-252-991A-4198	Sequence 4198, Ap
7	85.8	1.2	1824	4	US-09-252-991A-1780	Sequence 1780, Ap
8	83.8	1.2	1176	4	US-09-252-991A-3704	Sequence 3704, Ap
c 9	83.8	1.2	2253	4	US-09-252-991A-3810	Sequence 3810, Ap
10	81	1.2	36181	4	US-08-311-731A-120	Sequence 120, App
11	78.4	1.1	1548	4	US-09-252-991A-3653	Sequence 3653, Ap
c 12	77.4	1.1	762	4	US-09-252-991A-1938	Sequence 1938, Ap
c 13	76.6	1.1	4411529	3	US-09-103-840A-1	Sequence 1, Appli
14	75.2	1.1	969	4	US-09-107-532A-1008	Sequence 1008, Ap
15	75	1.1	1770	4	US-09-328-352-3466	Sequence 3466, Ap

SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
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4	636.6	9.3	854	12	BI854140	BI854140 603381449
5	624.4	9.1	754	14	CD351847	CD351847 UI-M-GIO-
c 6	591.2	8.6	878	12	BI182779	BI182779 UNL-P-FN-
7	587.8	8.5	673	14	CD351490	CD351490 UI-M-GIO-
c 8	550.4	8.0	661	14	CB481810	CB481810 jns83_A02
9	547.6	8.0	773	14	CB526974	CB526974 UI-M-FY0-
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16	516	7.5	620	14	CA889361	CA889361 B0152D10-
17	510.4	7.4	512	13	BX279856	BX279856 BX279856
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RESULT 1

AK051920

LOCUS AK051920 4783 bp mRNA linear HTC 05-DEC-2002
 DEFINITION Mus musculus 12 days embryo eyeball cDNA, RIKEN full-length
 enriched library, clone:D230019D04 product:ATP-binding cassette,
 sub-family A (ABC1), member 1, full insert sequence.

ACCESSION AK051920

VERSION AK051920.1 GI:26342297

KEYWORDS HTC; CAP trapper.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1
AUTHORS Carninci, P. and Hayashizaki, Y.
TITLE High-efficiency full-length cDNA cloning
JOURNAL Meth. Enzymol. 303, 19-44 (1999)
MEDLINE 99279253
PUBMED 10349636

REFERENCE 2
AUTHORS Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
TITLE Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL Genome Res. 10 (10), 1617-1630 (2000)
MEDLINE 20499374
PUBMED 11042159

REFERENCE 3
AUTHORS Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,
Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M.,
Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,
Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,
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TITLE RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer
JOURNAL Genome Res. 10 (11), 1757-1771 (2000)
MEDLINE 20530913
PUBMED 11076861

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AUTHORS Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y.,
Arakawa, T., Hara, A., Fukunishi, Y., Konno, H., Adachi, J., Fukuda, S.,
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Fleischmann, W., Gaasterland, T., Gissi, C., King, B., Kochiwa, H.,
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Hofmann, M., Hume, D. A., Kamiya, M., Lee, N. H., Lyons, P.,
Marchionni, L., Mashima, J., Mazzarelli, J., Mombaerts, P., Nordone, P.,
Ring, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H.,
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Toyo-oka, K., Wang, K. H., Weitz, C., Whittaker, C., Wilming, L.,
Wynshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawaji, H., Kohtsuki, S.
and Hayashizaki, Y.
TITLE Functional annotation of a full-length mouse cDNA collection
JOURNAL Nature 409 (6821), 685-690 (2001)
MEDLINE 21085660
PUBMED 11217851

REFERENCE 5
AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research
Group Phase I & II Team.
TITLE Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
JOURNAL Nature 420, 563-573 (2002)
REFERENCE 6 (bases 1 to 4783)
AUTHORS Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P.,
Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W.,
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Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S.,

Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A.,
Muramatsu,M. and Hayashizaki,Y.

TITLE Direct Submission

JOURNAL Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
Fax:81-45-503-9216)

COMMENT cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Please visit our web site for further details.
URL:http://genome.gsc.riken.go.jp/
URL:http://fantom.gsc.riken.go.jp/.

FEATURES Location/Qualifiers

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ORIGIN

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Matches 3901; Conservative 0; Mismatches 501; Indels 0; Gaps 0;

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Db	2422	GTGGTCATCTTGAAGTTAGGAAACCTGCTGCCCTATAGTGACCCCAGCGTGGTGTGTC	2481
Qy	2101	TTCTGTGCCGTGTTTGCTGTGGTGACAATCCTGCAGTGCTTCTGATTAGCACACTCTTC	2160
Db	2482	TTCTGTCTGTGTTTGCCATGGTGACCATCTACAGTGCTTCTCTATTAGCAGCTCTTC	2541

Qy	2161	TCCAGAGCCAACCTGGCAGCAGCCTGTGGGGGCATCATCTACTTCACGCTGTACCTGCCC	2220
Db	2542		2601
Qy	2221	TACGTCCTGTGTGTGGCATGGCAGGACTACGTGGGCTTCACACTCAAGATCTTCGCTAGC	2280
Db	2602		2661
Qy	2281	TATGTGCTGTGCGTAGCCTGGCAGGACTATGTGGGCTTCTCCATCAAGATCTTTGCTAGC	2340
Db	2662		2721
Qy	2341	CTGCTGTCTCCTGTGGCTTTTGGGTTTGGCTGTGAGTACTTTGCCCTTTTTCGAGGAGCAG	2400
Db	2722		2781
Qy	2401	GGCATTGGAGTGCAGTGGGACAACTGTTTGAGAGTCTCTGTGGAGGAAGATGGCTTCAAT	2460
Db	2782		2841
Qy	2461	GGTATCGGGGTCCAATGGGACAATCTCTTTGAGAGCCCGGTGGAGGAGGACGGCTTCAAT	2520
Db	2842		2901
Qy	2521	CTCACCACCTTCGGTCTCCATGATGCTGTTTGACACCTTCTCTATGGGGTGATGACCTGG	2580
Db	2902		2961
Qy	2581	CTCACCACCTGCAGTGTCATGATGCTCTTTGACACCTTCTCTATGGCGTGATGACATGG	2640
Db	2962		3021
Qy	2641	TACATTGAGGCTGTCTTTCCAGGCCAGTACGGAATTCACAGCCCTGGTATTTTCCTTGC	2700
Db	3022		3081
Qy	2701	TACATCGAAGCCGTCTTTCCAGGACAGTATGGAATTCACAGCCCTGGTATTTTCCTTGT	2760
Db	3082		3141
Qy	2761	ACCAAGTCCTACTGGTTTGGCGAGGAAAGTGATGAGAAGAGCCACCCTGGTTCCAACCAG	2820
Db	3142		3201
Qy	2821	ACCAAGTCATACTGGTTTGGTGAGGAAATTGATGAGAAGAGCCACCCTGGTTCCAGCCAG	2880
Db	3202		3261
Qy	2881	AAGAGAATATCAGAAATCTGCATGGAGGAGGAACCCACCCACTTGAAGCTGGGCGTGCC	2940
Db	3262		3321
Qy	2941	AAGGGAGTGTCAGAAATCTGCATGGAAGAGGAACCCACTCATCTGAGGCTGGGGGTGTC	3000
Db	3322		3381
Qy	3001	CTGAATTTTATGAGGGCCAGATCACCTCCTTCCTGGGCCACAATGGAGCGGGGAAGACG	3060
Db	3382		3441
Qy	3061	CTCAACTTTTACGAAGGCCAGATTACCTCCTTCCTGGGCCACAATGGAGCAGGGAAGACC	3120
Db	3442		3501
Qy	3121	ACCACCATGTCAATCCTGACCGGGTTGTTCCCCCGACCTCGGGCACCGCCTACATCCTG	3180
Db	3502		3561
Qy	3181	ACCACCATGTCAATACTGACTGGGCTGTTTCCCCCAACTTCTGGGCACGGCCTACATCCTG	3240
Qy	3241	GGAAAAGACATTTCGCTCTGAGATGAGCACCATCCGGCAGAACCTGGGGGTCTGTCCCCAG	3300
Db	3562		3621
Qy	3281	GGGAAGGACATTTCGCTCGGAGATGAGCTCCATCCGGCAGAACCTGGGAGTCTGTCCCCAG	3360
Db	3622		3681
Qy	3321	CATAACGTGCTGTTTGACATGCTGACTGTGCGAAGAACACATCTGGTTCTATGCCCGCTTG	3400
Db	3682		3741
Qy	3361	CATAATGTGCTGTTTGACATGCTGACTGTGCGAAGAGACATCTGGTTCTATGCGCGCTA	3440
Db	3742		3801
Qy	3401	AAAGGGCTCTCTGAGAAGCACGTGAAGGCGGAGATGGAGCAGATGGCCCTGGATGTTGGT	3500
Db	3802		3861
Qy	3441	AAGGGGCTCTCAGAGAAGCACGTGAAAGCAGAGATGGAGCAGATGGCCCTGGATGTTGGC	3540
Db	3862		3901
Qy	3481	TTGCCATCAAGCAAGCTGAAAAGCAAAACAAGCCAGCTGTGAGGTGGAATGCAGAGAAAG	3600
Db	3902		3661
Qy	3521	TTACCCCCGAGCAAGCTGAAAAGCAAAACGAGTCAGCTCTCAGGTGGGATGCAGAGAAAG	3640
Db	3962		3701
Qy	3561	CTATCTGTGGCCTTGGCCTTTGTCTGGGGGATCTAAGGTTGTCAATTCTGGATGAACCCACA	3720
Db	3962		3781
Qy	3601	CTGTCTGTGGCCTTGGCCTTCGTGGGTGGATCCAAGGTTGTCAATTCTGGACGAGCCACA	3760
Db	3962		3821
Qy	3641	GCTGGTGTGGACCCCTTACTCCCGCAGGGGAATATGGGAGCTGCTGCTGAAATACCGACAA	3800
Db	3962		3861
Qy	3681	GCCGGGGTGGACCCGTACTCTCGCAGGGGAATATGGGAACCTCTGCTAAAATACCGGCAA	3840
Db	3962		3901
Qy	3721	GGCCGCACCATATTCTCTCTACACACCACATGGATGAAGCGGACGTCCTGGGGGACAGG	3920
Db	3962		3981

Db	3562	GGCCGCACCATTATTTTGTCTACACACCACATGGACGAAGCTGACATCCTTGGGGACAGA	3621
Qy	3241	ATTGCCATCATCTCCCATGGGAAGCTGTGCTGTGTGGGCTCCTCCCTGTTTCTGAAGAAC	3300
Db	3622	ATTGCCATCATTTCATGGGAAGCTGTGTTGTGTGGGCTCCTCCCTGTTTGTGAAAAAC	3681
Qy	3301	CAGCTGGGAACAGGCTACTACCTGACCTTGGTCAAGAAAGATGTGGAATCCTCCCTCAGT	3360
Db	3682	CAGTTGGGAACGGGTTACTATCTGACCTTGGTTAAGAAAGATGTGGAATCGTCCCTCAGT	3741
Qy	3361	TCCTGCAGAAACAGTAGTAGCACTGTGTCATACCTGAAAAAGGAGGACAGTGTTCCTCAG	3420
Db	3742	TCCTGCAGAAACAGTAGCAGCACCGTGTCTTGTCTGAAAAAGGAGGACAGTGTTCCTCAG	3800
Qy	3421	AGCAGTTCTGATGCTGGCCTGGGCAGCGACCATGAGAGTGACACGCTGACCATCGATGTC	3480
Db	3802	AGCAGTTCTGATGCTGGCCTGGGCAGCGACCATGAAAGTGACACGCTGACCATCGATGTC	3861
Qy	3481	TCTGCTATCTCCAACCTCATCAGGAAGCATGTGTCTGAAGCCCGGCTGGTGGAAGACATA	3540
Db	3862	TCTGCTATCTCCAACCTCATCAGGAAGCACGTGTCTGAAGCCCGGCTGGTGGAAGACATT	3921
Qy	3541	GGGCATGAGCTGACCTATGTGCTGCCATATGAAGCTGCTAAGGAGGGAGCCTTGTGGAA	3600
Db	3922	GGGCACGAGCTGACCTATGTGCTGCCGTACGAAGCCGCGAAGGAGGGAGCCTTGTGGAA	3981
Qy	3601	CTCTTTCATGAGATTGATGACCGGCTCTCAGACCTGGGCATTCTAGTTATGGCATCTCA	3660
Db	3982	CTCTTCCATGAGATTGATGACCGGCTCTCAGACCTGGGCATCTCCAGTTATGGCATCTCG	4041
Qy	3661	GAGACGACCCTGGAAGAAATATTCTCTCAAGGTGGCCGAAGAGAGTGGGGTGGATGCTGAG	3720
Db	4042	GAGACCACCCTGGAAGAAATATTCTCTCAAGTGGCTGAAGAGAGCGGGGTGGATGCTGAG	4101
Qy	3721	ACCTCAGATGGTACCTTGCCAGCAAGACGAAACAGGCGGGCCTTCGGGGACAAGCAGAGC	3780
Db	4102	ACCTCAGATGGTACTTTGCCAGCAAGACGAAACAGACGGGCCTTCGGGGACAAGCAGAGC	4161
Qy	3781	TGTCTTCGCCCCGTTCACTGAAGATGATGCTGCTGATCCAAATGATTCTGACATAGACCCA	3840
Db	4162	TGTCTGCACCCATTTACGGAAGATGATGCTGTTGATCCCAATGACTCTGACATAGACCCA	4221
Qy	3841	GAATCCAGAGAGACAGACTTGCTCAGTGGGATGGATGGCAAAGGGTCTACCAGGTGAAA	3900
Db	4222	GAATCCAGGGAGACCGACCTGCTCAGTGGGATGGACGGCAAAGGGTCTACCAGCTGAAG	4281
Qy	3901	GGCTGGAAACTTACACAGCAACAGTTTGTGGCCCTTTTGTGGAAGAGACTGCTAATTGCC	3960
Db	4282	GGCTGGAAACTCACCCAGCAACAGTTTGTGGCCCTTTTGTGGAAGAGGCTGCTGATTGCC	4341
Qy	3961	AGACGGAGTCGAAAGGATTTTGTGCTCAGATTGTCTTGCCAGCTGTGTTTGTCTGCATT	4020
Db	4342	AGACGGAGCCGGAAGGTTTCTTTGCTCAGATTGTCTTGCCAGCTGTCTTGTGTTTGATT	4401
Qy	4021	GCCCTTGTGTTTCACTGATCGTGCCACCCTTTGGCAAGTACCCAGCCTGGAACCTTCAG	4080
Db	4402	GCCCTGGTCTTTCAGCTGATTGTGCCACCCTTTGGCAAGTACCCAGCCTGGAACCTTCAG	4461
Qy	4081	CCCTGGATGTACAACGAACAGTACACATTTGTGAGCAATGATGCTCCTGAGGACACGGGA	4140
Db	4462	CCCTGGATGTATAATGAGCAGTATACATTTGTGAGTAATGATGCTCCCGAGGACATGGGC	4521
Qy	4141	ACCCTGGAACCTCTTAAACGCCCTCACCAAAGACCCTGGCTTCGGGACCCGCTGTATGGAA	4200
Db	4522	ACCAGGAACCTCTGAATGCTCTGACCAAAGATCCAGGCTTTGGGACCCGCTGTATGGAA	4581
Qy	4201	GGAAACCCAATCCAGACACGCCCTGCCAGGCAGGGGAGGAAGAGTGGACCACTGCCCCA	4260
Db	4582	GGAAACCCAATCCAGATACCCCTTGCTTGGCTGGGGAGGAGGACTGGACCATCAGCCCC	4641
Qy	4261	GTTCCCCAGACCATCATGGACCTCTTCCAGAATGGGAACTGGACAATGCAGAACCCCTTCA	4320

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Db      4642  GTCCCCCAGAGCATCGTGGACCTCTTCCAGAATGGAACTGGACCATGAAGAACCCTCA 4701
Qy      4321  CCTGCATGCCAGTGTAGCAGCGACAAAAATCAAGAAGATGCTGCCTGTGTGTCCCCCAGGG 4380
Db      4702  CCTGCGTGCCAGTGTAGCAGTGACAAAAATCAAGAAGATGCTGCCTGTGTGTCCCCCAGGG 4761
Qy      4381  GCAGGGGGGCTGCCTCCTCCAC 4402
Db      4762  GCAGGGGGGCTGCCACCTCTC 4783

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SEQ ID NO: 2

Result No.	Score	Query Match	Length	DB	ID	Description
1	11469	100.0	2201	21	AAV79380	Human ATP binding
2	11469	100.0	2201	22	AAE13021	Human ATP binding
3	11469	100.0	2201	22	AAM50227	Human ATP binding
4	11469	100.0	2201	23	ABP65164	Hypoxia-regulated
5	11469	100.0	2261	22	AAE13022	Human ATP binding
6	11469	100.0	2261	22	AAM50228	Human ATP binding
7	11469	100.0	2261	22	AAU02176	Human ABC1. Homo
8	11469	100.0	2261	22	AAU02177	Human ABC1 mutant
9	11469	100.0	2261	23	ABB83111	Human ABCA1 transp
10	11469	100.0	2261	23	ABP52092	Homo sapiens ABC t
11	11469	100.0	2261	23	AAE23000	Human ABC1 full-le
12	11468	100.0	2261	23	ABB83117	Polymorphic human
13	11468	100.0	2261	23	ABB83124	Polymorphic human
14	11466	100.0	2261	22	AAU02183	Human ABC1 mutant
15	11466	100.0	2261	22	AAU02188	Human ABC1 mutant
16	11466	100.0	2261	23	ABB83115	Polymorphic human
17	11466	100.0	2261	23	ABB83116	Polymorphic human
18	11466	100.0	2261	23	ABB83119	Polymorphic human
19	11466	100.0	2261	23	ABB83122	Polymorphic human
20	11466	100.0	2261	23	ABB83123	Polymorphic human
21	11465	100.0	2261	22	AAU02189	Human ABC1 mutant
22	11464	100.0	2261	23	ABB83121	Polymorphic human
23	11463	99.9	2261	22	AAU02181	Human ABC1 mutant
24	11462	99.9	2261	22	AAM78550	Human protein SEQ
25	11462	99.9	2263	22	ABB11956	Human ABCA1 homolo
26	11462	99.9	2263	22	AAM79534	Human protein SEQ
27	11461	99.9	2261	22	AAU02182	Human ABC1 mutant
28	11461	99.9	2261	22	AAU02186	Human ABC1 mutant
29	11459	99.9	2261	23	ABB83118	Polymorphic human
30	11458	99.9	2261	23	ABB83120	Polymorphic human
31	11440	99.7	2261	21	AAB38082	Human ABC1 cholest
32	11440	99.7	2261	22	AAB71749	Human ABC1 protein
33	11440	99.7	2261	24	ABU11899	Human ATP-binding
34	11439	99.7	2261	23	ABB81578	Human ABC-A-1-1 pr
35	11437	99.7	2261	21	AAB38109	Human ABC1 cholest
36	11437	99.7	2261	21	AAB38111	Human ABC1 cholest
37	11437	99.7	2261	21	AAB38114	Human ABC1 cholest
38	11437	99.7	2261	21	AAB38115	Human ABC1 cholest
39	11437	99.7	2261	21	AAB38117	Human ABC1 cholest

No.	Score	Match	Length	DB	ID	Description
1	6909	60.2	1375	3	US-08-665-259-26	Sequence 26, Appl
2	6909	60.2	1375	3	US-08-762-500-26	Sequence 26, Appl
3	3129.5	27.3	1457	3	US-08-665-259-27	Sequence 27, Appl
4	3129.5	27.3	1457	3	US-08-762-500-27	Sequence 27, Appl
5	2635.5	23.0	1684	3	US-08-665-259-25	Sequence 25, Appl
6	2635.5	23.0	1684	3	US-08-762-500-25	Sequence 25, Appl
7	2635.5	23.0	1704	3	US-08-762-500-75	Sequence 75, Appl

8	359	3.1	315	4	US-09-328-352-4388	Sequence 4388, Ap
9	354	3.1	332	4	US-09-107-532A-3752	Sequence 3752, Ap
10	352.5	3.1	335	4	US-09-252-991A-20837	Sequence 20837, A
11	352	3.1	322	4	US-09-107-532A-4662	Sequence 4662, Ap
12	346	3.0	589	4	US-09-328-352-7592	Sequence 7592, Ap
13	336.5	2.9	1280	2	US-08-583-276-19	Sequence 19, Appl
14	335.5	2.9	291	4	US-09-107-532A-4205	Sequence 4205, Ap
15	335.5	2.9	1280	4	US-09-767-594-2	Sequence 2, Appli
16	335.5	2.9	1280	6	5206352-4	Patent No. 5206352
17	333	2.9	1279	2	US-08-784-649A-2	Sequence 2, Appli
18	332	2.9	402	4	US-09-107-532A-5360	Sequence 5360, Ap
19	330.5	2.9	1280	2	US-08-752-447-2	Sequence 2, Appli

RESULT 1

US-08-665-259-26

; Sequence 26, Application US/08665259

; Patent No. 6028173

; GENERAL INFORMATION:

; APPLICANT: Landes, Gregory M.

; APPLICANT: Burn, Timothy C.

; APPLICANT: Connors, Timothy D.

; APPLICANT: Dackowski, William R.

; APPLICANT: Van Raay, Terence J.

; APPLICANT: Klinger, Katherine W.

; TITLE OF INVENTION: NOVEL HUMAN CHROMOSOME 16 GENES,

; TITLE OF INVENTION: COMPOSITIONS, METHODS OF MAKING AND USING SAME

; NUMBER OF SEQUENCES: 73

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: GENZYME CORPORATION

; STREET: One Mountain Road

; CITY: Framingham

; STATE: Massachusetts

; COUNTRY: United States of America

; ZIP: 01701

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/665,259

; FILING DATE: 17-JUN-1996

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Dugan, Deborah A.

; REGISTRATION NUMBER: 37,315

; REFERENCE/DOCKET NUMBER: IG5-9.1

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (508) 872-8400

; TELEFAX: (508) 872-5415

; INFORMATION FOR SEQ ID NO: 26:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1375 amino acids

; TYPE: amino acid

; STRANDEDNESS: not relevant

; TOPOLOGY: unknown

; MOLECULE TYPE: protein

US-08-665-259-26

Query Match 60.2%; Score 6909; DB 3; Length 1375;

Best Local Similarity 96.9%; Pred. No. 0;

Matches 1332; Conservative 21; Mismatches 22; Indels 0; Gaps 0;

Qy 827 CMEEEPHTLKLGVSIQNLVKVYRDGMKVAVDGLALNFYEGQITSFLGHNGAGKTTTMSIL 886

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Db 1 CMEEEPHTLRLGVSIQNLVKVYRDGMKVAVDGLALNFYEGQITSFLGHNGAGKTTTMSIL 60

Qy 887 TGLFPPTSGTAYILGKDIRSEMSTIRQNLGVCPQHNVLFDMLTVEEHIWFYARLKLGLSEK 946

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Db 61 TGLFPPTSGTAYILGKDIRSEMSSIRQNLGVCQHNVLFDMLTVEEHIWFYARLKGLSEK 120
 Qy 947 HVKAEMEQMALDVGLPSSKLKSKTSQLSGGMQRKLSVALAFVGGSKVVILDEPTAGVDPY 1006
 Db 121 HVKAEMEQMALDVGLPSSKLKSKTSQLSGGMQRKLSVALAFVGGSKVVILDEPTAGVDPY 180
 Qy 1007 SRRGIWELLKRYQGRITILSTHHMDEADVLDRIAIISHGKLCCVGSSFLKNQLGTGY 1066
 Db 181 SRRGIWELLKRYQGRITILSTHHMDEADVLDRIAIISHGKLCCVGSSFLKNQLGTGY 240
 Qy 1067 YLTLVKKDVESLSSCRNSSSTVSYLKEDSVSQSSDAGLGDHESDTLTIDVSAISNL 1126
 Db 241 YLTLVKKDVESLSSCRNSSSTVSLKEDSVSQSSDAGLGDHESDTLTIDVSAISNL 300
 Qy 1127 IRKHVSEARLVEDIGHELTYVLPYAAKEGAFVELFHEIDRLSDLGISYGISETTLEE 1186
 Db 301 IRKHVSEARLVEDIGHELTYVLPYAAKEGAFVELFHEIDRLSDLGISYGISETTLEE 360
 Qy 1187 IFLKVAESGVDAETSDGTLPARNRRAFGDKQSCLRPFTEDDAADPNDSIDPESRETD 1246
 Db 361 IFLKVAESGVDAETSDGTLPARNRRAFGDKQSCLHPFTEDDAVDPNDSIDPESRETD 420
 Qy 1247 LLSGMDGKGSYQVKGWLTQQQFVALLWKRLLIARRSRKGFFAQIVLPAVFCIALVFSL 1306
 Db 421 LLSGMDGKGSYQLKGWLTQQQFVALLWKRLLIARRSRKGFFAQIVLPAVFCIALVFSL 480
 Qy 1307 IVPFPGKYPSLELQPMWYNEQYTFVNSDAPEDTGTLELLNALTDPGFGTRCMEGNPID 1366
 Db 481 IVPFPGKYPSLELQPMWYNEQYTFVNSDAPEDMGTQELLNALTDPGFGTRCMEGNPID 540
 Qy 1367 TPCQAGEEWTTPVPQTIMDLFQNGNWTMKNPSPACQCSSDKIKKMLPVCPPGAGGLPP 1426
 Db 541 TPCQAGEEDWTISPVQSIQVDFQNGNWTMKNPSPACQCSSDKIKKMLPVCPPGAGGLPP 600
 Qy 1427 PQRKQNTADILQDLTGRNISDYLVKTYVQIIAKSLKNKIWNNEFRYGGFSLGVSNTQALP 1486
 Db 601 PQRKQNTADILQDLTGRNISDYLVKTYVQIIAKSLKNKIWNNEFRYGGFSLGVSNTQALP 660
 Qy 1487 PSQEVNDATKQMKKHLKLAKDSSADRFNLNLSGRFMTGLDTRNNVKVWFNNKGWHAISSFL 1546
 Db 661 PSQEVNDATKQMKKHLKLAKDSSADRFNLNLSGRFMTGLDTRNNVKVWFNNKGWHAISSFL 720
 Qy 1547 NVINNAILRANLQKGENPSHYGITAFNHPLNLTQQLSEVAPMTTSVDVLVSICVIFAMS 1606
 Db 721 NVINNAILRANLQKGENPSHYGITAFNHPLNLTQQLSEVAPMTTSVDVLVSICVIFAMS 780
 Qy 1607 FVPASFVFLIQUERVSKAKHLQFISGVKPIYWLNSFVWDMCNYVVPATLVIIIFICFQQ 1666
 Db 781 FVPASFVFLIQUERVSKAKHLQFISGVKPIYWLNSFVWDMCNYVVPATLVIIIFICFQQ 840
 Qy 1667 KSYVSSTNLPVLALLLLLYGWSITPLMPASFVFKIPSTAYVVLTSVNLFIGINGSVATF 1726
 Db 841 KSYVSSTNLPVLALLLLLYGWSITPLMPASFVFKIPSTAYVVLTSVNLFIGINGSVATF 900
 Qy 1727 VLELFTDNKLNNINDILKSVFLIFPHFCLGRGLDMVKNQAMADALERFGENRFVSPLSW 1786
 Db 901 VLELFTDNKLNNINDILKSVFLIFPHFCLGRGLDMVKNQAMADALERFGENRFVSPLSW 960
 Qy 1787 DLVGRNLFAMAVEGVVFLITVLIQYRFFIRPRPVNAKLSPLNDEDEDVRRERQRILDGG 1846
 Db 961 DLVGRNLFAMAVEGVVFLITVLIQYRFFIRPRPVNAKLSPLNDEDEDVRRERQRILDGG 1020
 Qy 1847 GQNDILEIKELTKIYRRKRKPAVDRICIGIPPGEFCGLLGNGAGKSTTFKMLTGDTPVT 1906
 Db 1021 GQNDILEIKELTKIYRRKRKPAVDRICIGIPPGEFCGLLGNGAGKSTTFKMLTGDTPVT 1080
 Qy 1907 RGDAFLNRNSILSNIHEVHQNMGYCPQFDAITELLTGREHVEFFALLRGVPEKEVGKVE 1966
 Db 1081 RGDAFLNRNSILSNIHEVHQNMGYCPQFDAITELLTGREHVEFFALLRGVPEKEVGKVE 1140
 Qy 1967 WAIRKGLVKYGEKYAGNYSNGGNKRKLSTAMALIGPPVFLDEPTTGMDPKARRFLWNC 2026

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Db      1141  WAIRKRLGLVKYGEKYASNYSGGNKRKLSTAMALIGGPPVFLDEPTTGMDPKARRFLWNC 1200
Qy      2027  ALSVVKEGRSVVLTSHSMEECEALCTRMALMVNGRFRCLGSLVQHLKNRFGDGYTIVVRIA 2086
Db      1201  ALSIVKEGRSVVLTSHSMEECEALCTRMALMVNGRFRCLGSLVQHLKNRFGDGYTIVVRIA 1260
Qy      2087  GSNPDLKPVQDFGLAFPGSVPEKHRNMLQYQLPSSLSLARIFSILSQSKKRLHIEDY 2146
Db      1261  GSNPDLKPVQEFFGLAFPGSVLKEKHRNMLQYQLPSSLSLARIFSILSQSKKRLHIEDY 1320
Qy      2147  SVSQTTLDQVFNFAKDQSDDDLKDLKSLHKNQTVVDVAVLTSFLQDEKVKESYV 2201
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RESULT 2

US-08-762-500-26

; Sequence 26, Application US/08762500

; Patent No. 6030806

; GENERAL INFORMATION:

; APPLICANT: Landes, Gregory M.

; APPLICANT: Burn, Timothy C.

; APPLICANT: Connors, Timothy D.

; APPLICANT: Dackowski, William R.

; APPLICANT: Van Raay, Terence J.

; APPLICANT: Klinger, Katherine W.

; TITLE OF INVENTION: NOVEL HUMAN CHROMOSOME 16 GENES,

; TITLE OF INVENTION: COMPOSITIONS, METHODS OF MAKING AND USING SAME

; NUMBER OF SEQUENCES: 83

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: GENZYME CORPORATION

; STREET: One Mountain Road

; CITY: Framingham

; STATE: Massachusetts

; COUNTRY: United States of America

; ZIP: 01701

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/762,500

; FILING DATE: 09-DEC-1996

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/665,259

; FILING DATE: 17-JUN-1996

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: PCT/US96/10469

; FILING DATE: 17-JUN-1996

; ATTORNEY/AGENT INFORMATION:

; NAME: Dugan, Deborah A.

; REGISTRATION NUMBER: 37,315

; REFERENCE/DOCKET NUMBER: IG5-9.3

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (508) 872-8400

; TELEFAX: (508) 872-5415

; INFORMATION FOR SEQ ID NO: 26:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1375 amino acids

; TYPE: amino acid

; STRANDEDNESS: not relevant

; TOPOLOGY: unknown

; MOLECULE TYPE: protein

US-08-762-500-26

Query Match

60.2%; Score 6909; DB 3; Length 1375;

Best Local Similarity 96.9%; Pred. No. 0;
Matches 1332; Conservative 21; Mismatches 22; Indels 0; Gaps 0;

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Qy      827 CMEEEPHTHLKLGVSIGNLVKQYRDGMKVAVDGLALNFYEGQITSFLGHNGAGKTTTMSIL 886
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Db      1 CMEEEPHTHLRLGVSIGNLVKQYRDGMKVAVDGLALNFYEGQITSFLGHNGAGKTTTMSIL 60

Qy      887 TGLFPPTSGTAYILGKDIRSEMSTIRQNLGVCPQHNVLFDMLTVEEHIWIFYARLKGLSEK 946
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      61 TGLFPPTSGTAYILGKDIRSEMSSIRQNLGVCPQHNVLFDMLTVEEHIWIFYARLKGLSEK 120

Qy      947 HVKAEMEQLMALDVGLPSSKLKSKTSQLSGGMQRKLSVALAFVGGSKVVILDEPTAGVDPY 1006
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      121 HVKAEMEQLMALDVGLPSSKLKSKTSQLSGGMQRKLSVALAFVGGSKVVILDEPTAGVDPY 180

Qy     1007 SRRGIWELLKRYRQGRTIILSTHMHDEADVLDRIAIIISHGKLCCVSSFLKNQLGTGY 1066
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      181 SRRGIWELLKRYRQGRTIILSTHMHDEADILGDRIAIIISHGKLCCVSSFLKNQLGTGY 240

Qy     1067 YLTLVKKDVESLSSCRNSSSTVSYLKKEDSVSQSSDAGLGDHESDTLTIDVSAISNL 1126
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      241 YLTLVKKDVESLSSCRNSSSTVSLCKEDSVSQSSDAGLGDHESDTLTIDVSAISNL 300

Qy     1127 IRKHVSEARLVEDIGHELTYVLPYEAKEGAFVELFHEIDRLSDLGISYGISETTLEE 1186
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      301 IRKHVSEARLVEDIGHELTYVLPYEAKEGAFVELFHEIDRLSDLGISYGISETTLEE 360

Qy     1187 IFLKVAESGVDAETSDGTLPARNRRAFGDKQSCLRPFTEDDAADPNDSIDPESRETD 1246
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      361 IFLKVAESGVDAETSDGTLPARNRRAFGDKQSLHPFTEDDAVDPNDSIDPESRETD 420

Qy     1247 LLSGMDGKGSYQVKGWKLQQQFVALLWKRLLIARRSRKGFFAQIVLPAVFVCIALVFSL 1306
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      421 LLSGMDGKGSYQLKGWKLQQQFVALLWKRLLIARRSRKGFFAQIVLPAVFVCIALVFSL 480

Qy     1307 IVPFPGKYPSLELQPMWYNEQYTFVSNDAPEDTGTLELLNALT KD PGFGTRCMEGNPIPD 1366
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      481 IVPFPGKYPSLELQPMWYNEQYTFVSNDAPEDMGTQELNALT KD PGFGTRCMEGNPIPD 540

Qy     1367 TPCQAGEEETAPVPQTIMDLFQNGNWTMKNPSPACQCSSDKIKKMLPVCPPGAGGLPP 1426
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      541 TPCLAGEDWTISPVPQSI VDLFQNGNWTMKNPSPACQCSSDKIKKMLPVCPPGAGGLPP 600

Qy     1427 PQRKQNTADILQDLTGRNISDYLVKTYVQIIAKSLKNKIWNNEFRYGGFSLGVSNTQALP 1486
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      601 PQRKQKTADILQDLTGRNISDYLVKTYVQIIAKSLKNKIWNNEFRYGGFSLGVSNSQALP 660

Qy     1487 PSQEVNDATKQMKKHLKLAKDSSADRFLNSLGRFMTGLDTRNNVKVWFNNKGWHAISSFL 1546
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      661 PSHEVNDATKQMKKLLKLT KDTSADRFLSSLGRFMAGLDTKNNVKVWFNNKGWHAISSFL 720

Qy     1547 NVINNAILRANLQKGENPSHYGITAFNHPLNLTQQLSEVAPMTTSVDVLVSICVIFAMS 1606
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      721 NVINNAILRANLQKGENPSQYGITAFNHPLNLTQQLSEVALMTTSVDVLVSICVIFAMS 780

Qy     1607 FVPASFVFLIQERVSKAKHLQFISGVKPVYIWLNSFVWDMCNYVVPATLVIIIFICFQQ 1666
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      781 FVPASFVFLIQERVSKAKHLQFISGVKPVYIWLNSFVWDMCNYVVPATLVIIIFICFQQ 840

Qy     1667 KSYVSSTNLPVLALLLLLYGWSITPLMPASFVFKIPSTAYVVLTSVNLFIGINGSVATF 1726
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      841 KSYVSSTNLPVLALLLLLYGWSITPLMPASFVFKIPSTAYVVLTSVNLFIGINGSVATF 900

Qy     1727 VLELFTDNKLNNDILKSVFLIFPHFCLGRGLIDMVKNQAMADALERFGENRFVSPLSW 1786
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      901 VLELFTNNKLNNDILKSVFLIFPHFCLGRGLIDMVKNQAMADALERFGENRFVSPLSW 960

Qy     1787 DLVGRNLFAMAVEGVVFLITVLIQYRFFIRPRPVNAKLSPLNDEDEDVRRERQRILDGG 1846
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      961 DLVGRNLFAMAVEGVVFLITVLIQYRFFIRPRPVNAKLPPLNDEDEDVRRERQRILDGG 1020
```


Qy	1847	GQNDILEIKELTKIYRRKRKPAVDRICVGIPPGECFGLLGVNGAGKSSTFKMLTGDTTVT	1906
Db	1021	GQNDILEIKELTKIYRRKRKPAVDRICIGIPPGECFGLLGVNGAGKSTTFKMLTGDTPVT	1080
Qy	1907	RGDAFLNRNSILSNIHEVHQNMGYCPQFDAITELLTGREHVEFFALLRGVPEKEVGKVGE	1966
Db	1081	RGDAFLNKNSILSNIHEVHQNMGYCPQFDAITELLTGREHVEFFALLRGVPEKEVGKFGE	1140
Qy	1967	WAIRKLGVLVKYGEKYAGNYSGGNKRKLSTAMALIGPPVVFLDEPTTGMDPKARRFLWNC	2026
Db	1141	WAIRKLGVLVKYGEKYASNYSGGNKRKLSTAMALIGPPVVFLDEPTTGMDPKARRFLWNC	1200
Qy	2027	ALSVVKEGRSVVLTSHSMEECEALCTRMAIMVNGRFRCLGSVQHLKNRFGDGYTIVVRIA	2086
Db	1201	ALSIVKEGRSVVLTSHSMEECEALCTRMAIMVNGRFRCLGSVQHLKNRFGDGYTIVVRIA	1260
Qy	2087	GSNPDLKPVDFFGLAFPGSVPEKEHRNMLQYQLPSSLSSLARIFSILSQSKRRLHIEDY	2146
Db	1261	GSNPDLKPVQEFFGLAFPGSVLKEKHRNMLQYQLPSSLSSLARIFSILSQSKRRLHIEDY	1320
Qy	2147	SVSQTTLDQVFNFAKDQSDDDHLKDLSLHKNQTVVDVAVLTSFLQDEKVKESYV	2201
Db	1321	SVSOTTLDQVFNFAKDOSDDHLKDLSLHKNQTVVDVAVLTSFLQDEKVKESYV	1375

F;1869-2060/Domain: ATP-binding cassette homology <ABC2>
F;1886-1893/Region: nucleotide-binding motif A (P-loop)

Qy	1	MPSAGTLPWVQGIICNANNPCFRYPTPGEAPGVGNFNKSIVARLFS	DARRLLYSQKDT	60	
Db	1	MPSAGTLPWVQGIICNANNPCFRYPTPGEAPGVGNFNKSIVSR	LFSDAQRLLLSQRDT	60	
Qy	61	SMKDMRKVLRTLQQIKKSSSNLKLQDFLVDNETFSGFLYHNLSL	PKSTVDKMLRADVILH	120	
Db	61	SIKDMHKVLRMLRQIKHPNSNLKLQDFLVDNETFSGFLQHNLS	LPSTVDSLLQXNVGLQ	120	
Qy	121	KVFLQGYQLHLTSLCNGSKSEEMIQLGDQEVSEL	CGLPREKLAAERVLSNMDILKPIL	180	
Db	121	KVFLQGYQLHLASLCNGSKLEEIIQLGDAEVSALCGLPR	KKLDAAEVRLRYNMDILKPVV	180	
Qy	181	RTLNSTSPFPSKELAEATKTLHLSLGTLAQELFS	MRSWSDMRQEVMLFTNVN	240	
Db	181	TKLNSTSHLPTQHLAEATTVLLDSLGLLAQELF	STKSWSDMRQEVMLFTNVN	240	
Qy	241	YQAVSRIVCGHPEGGLKIKSLNWEYEDNNYKAL	FGNGTEEDAETFYDNSTTPYCNDLMK	300	
Db	241	YQAVSRIVCGHPEGGLKIKSLNWEYEDNNYKAL	FGGNTEEDVDTFYDNSTTPYCNDLMK	300	
Qy	301	NLESSPLSRIIWKALKPLLVGKILYTPDTPAT	RQVMAEVNKTQFELAVFHDLEGMWHEELS	360	
Db	301	NLESSPLSRIIWKALKPLLVGKILYTPDTPAT	RQVMAEVNKTQFELAVFHDLEGMWHEELS	360	
Qy	361	PKIWTFMENSQEMDLVRMLLDSRDNDHFWEQ	QLDGLDWTAQDIVAFLAKHPEDVQSSNGS	420	
Db	361	PQIWTFMENSQEMDLVRTLLDSRGNDQFWEQ	KLDGLDWTAQDIMAFLAKNPEDVQSPNGS	420	
Qy	421	VYTWEAFNETNQAIRTISRFMECVNLNKLEPI	ATEVWLINKSMELLDERKF	WAGIVFTG	480
Db	421	VYTWEAFNETNQAIQTISRFMECVNLNKLEPI	TEVRLINKSMELLDERKF	WAGIVFTG	480
Qy	481	ITPGSIELPHHVYKIRMDIDNVERTNKIKDGY	WDPGPRADPFEDMRYVWGGFAYLQDVV	540	
Db	481	ITPDSVELPHHVYKIRMDIDNVERTNKIKDGY	WDPGPRADPFEDMRYVWGGFAYLQDVV	540	
Qy	541	EQAIIRVLTGTEKKTGVYMQMPYPCYVDDIF	LRVMSRSMPLFMTLAWIYSVAVIK	GIV	600
Db	541	EQAIIRVLTGSEKKTGVYVQMPYPCYVDDIF	LRVMSRSMPLFMTLAWIYSVAVIK	SIV	600
Qy	601	YEKEARLKETMRIMGLDNLWFSWFISSLIPL	LVSVAGLLVVILKGNLLPYSDPSVVFV	660	
Db	601	YEKEARLKETMRIMGLDNGILWFSWFVSSLI	PLVSVAGLLVVILKGNLLPYSDPSVVFV	660	
Qy	661	FLSVFAVVTILQCFLISTLFSRANLAAACGG	IYFTLYLPYVLCVAWQDYVGF	TLKIFAS	720
Db	661	FLSVFAMVTILQCFLISTLFSRANLAAACGG	IYFTLYLPYVLCVAWQDYVGF	FSIKIFAS	720
Qy	721	LLSPVAFGFGCEYFALFEEQIGIGVQWDNL	FESPVEEDGFNLTTSVSMMLFDTFLYGV	MTW	780
Db	721	LLSPVAFGFGCEYFALFEEQIGIGVQWDNL	FESPVEEDGFNLTTAVSMMLFDTFLYGV	MTW	780
Qy	781	YIEAVFPQGYGIPRPWYFPCTKSYWFGES	DEKSHPGSNQKRRISEICMEEEP	THLKLGV	840
Db	781	YIEAVFPQGYGIPRPWYFPCTKSYWFGEE	IDKSHPGSSQKGVSEICMEEEP	THLRLGV	840
Qy	841	IQNLVKVYRDGMKVAVDGLALNFYEQITS	FGLHNGAGKTTTMSILTGLFPPTSGTAY	IL	900
Db	841	IQNLVKVYRDGMKVAVDGLALNFYEQITS	FGLHNGAGKTTTMSILTGLFPPTSGTAY	IL	900
Qy	901	GKDIRSEMSTIRQNLGVCPOHNVLFDM	LTVEEHIWIFYARLKGLSEKHVKAEME	QMALDVG	960
Db	901	GKDIRSEMSSIRQNLGVCPOHNVLFDM	LTVEEHIWIFYARLKGLSEKHVKAEME	QMALDVG	960

Qy	961	LPSSKLKSKTSQLSGGMQRKLSVALAFVGGSKVVILDEPTAGVDPYSRRGIWELLKYRQ	1020
Db	961	LPSSKLKSKTSQLSGGMQRKLSVALAFVGGSKVVILDEPTAGVDPYSRRGIWELLKYRQ	1020
Qy	1021	GRTIILSTHHMDEADVLDRIAIISHGKLCCVGSSFLKNQLGTGYLTLVKKDVESSL	1080
Db	1021	GRTIILSTHHMDEADILGDRIAIISHGKLCCVGSSFLKNQLGTGYLTLVKKDVESSL	1080
Qy	1081	SCRNSSSTVSYLKKEDSVSQSSSDAGLGDHESDTLTIDVSAISNLIRKXHVSEARLVEDI	1140
Db	1081	SCRNSSSTVSYLKKEDSVSQSSSDAGLGDHESDTLTIDVSAISNLIRKXHVSEARLVEDI	1140
Qy	1141	GHELTIVLPYEAKEGAFVELFHEIDRLSDLGISYGISETTLEEFLKVAEESGVDAE	1200
Db	1141	GHELTIVLPYEAKEGAFVELFHEIDRLSDLGISYGISETTLEEFLKVAEESGVDAE	1200
Qy	1201	TSDGTLPARRNRRAFGDKQSLRPFTEDDAADPNDSIDPESRETDLGMDGKGSYQVK	1260
Db	1201	TSDGTLPARRNRRAFGDKQSLRPFTEDDAADPNDSIDPESRETDLGMDGKGSYQVK	1260
Qy	1261	GWKLTQQQFVALLWKRLLIARRSRKGFQAIVLPAVFCIALVFSLIVPPFGKYPSELEQ	1320
Db	1261	GWKLTQQQFVALLWKRLLIARRSRKGFQAIVLPAVFCIALVFSLIVPPFGKYPSELEQ	1320
Qy	1321	PWYNEQYTFVSNDAPEDTGTLELLNALTCDPGFGRMEGNPIPDTPCQAGEEWTAP	1380
Db	1321	PWYNEQYTFVSNDAPEDMGTQELNALTCDPGFGRMEGNPIPDTPCLAGEEDWTISP	1380
Qy	1381	VPQITMDLFQNGNWTMKNPSPACQCSSDKIKMLPVCPPGAGGLPPPQRKQNTADILQDL	1440
Db	1381	VPQISVDLFQNGNWTMKNPSPACQCSSDKIKMLPVCPPGAGGLPPPQRKQNTADILQNL	1440
Qy	1441	TGRNISDYLKTYVQIIAKSLKNIWNEFRYGGFSLGVSNTQALPPSQEVNDATKQMKK	1500
Db	1441	TGRNISDYLKTYVQIIAKSLKNIWNEFRYGGFSLGVSNSQALPPSHEVNDAIKQMKK	1500
Qy	1501	HLKLAKDSSADRFLNSLGRFMTGLDTRNNVKVWFNNKGWHAISSFLNVINNAIRANLQK	1560
Db	1501	LLKLTKDTSADRFLSSLGRFMAGLDTKNNVKVWFNNKGWHAISSFLNVINNAIRANLQK	1560
Qy	1561	GENPSHYGITAFNHPLNLTQQLSEVAPMTTSVDVLVSICVIFAMSFVPASFVFLIQR	1620
Db	1561	GENPSYQGITAFNHPLNLTQQLSEVALMTTSVDVLVSICVIFAMSFVPASFVFLIQR	1620
Qy	1621	VSKAKHLQFISGVKPIYWLNSFVWDMCNVVPATLVIIIFICFQKQSYVSSTNLPVLAL	1680
Db	1621	VSKAKHLQFISGVKPIYWLNSFVWDMCNVVPATLVIIIFICFQKQSYVSSTNLPVLAL	1680
Qy	1681	LLLLYGSWITPLMPASFVFKIPSTAYVVLTSVNLFIGINGSVATFVLELFTDNKLNNIN	1740
Db	1681	LLLLYGSWITPLMPASFVFKIPSTAYVVLTSVNLFIGINGSVATFVLELFTNNKLNDIN	1740
Qy	1741	DILKSVFLIFPHFCLGRGLIDMVKNQAMADALERFGENRFVSPSWDLVGRNLFAMAVEG	1800
Db	1741	DILKSVFLIFPHFCLGRGLIDMVKNQAMADALERFGENRFVSPSWDLVGRNLFAMAVEG	1800
Qy	1801	VVFFLITVLIQYRFFIRPRPVNAKLSPLNDEDEDVRRERQRILDGGGQNDILEIKELTKI	1860
Db	1801	VVFFLITVLIQYRFFIRPRPVNAKLPPLNDEDEDVRRERQRILDGGGQNDILEIKELTKI	1860
Qy	1861	YRRKRKPAVDRICVGIIPPGEFCGLLGNGAGKSTTFKMLTGDTTVTRGDAFLNRNSILSN	1920
Db	1861	YRRKRKPAVDRICIGIIPPGEFCGLLGNGAGKSTTFKMLTGDTPVTRGDAFLNKNSILSN	1920
Qy	1921	IHEVHQNMGYCQFDAITELLTGREHVEFFALLRGVPEKEVGKVGGEWAIRKGLVKYGEK	1980
Db	1921	IHEVHQNMGYCQFDAITELLTGREHVEFFALLRGVPEKEVGKVGGEWAIRKGLVKYGEK	1980
Qy	1981	YAGNYSGGNKRKLSTAMALIGPPVVFLEPTTGMDPKARRFLWNCALSVVKEGRSVVLT	2040
Db	1981	YASNYSGGNKRKLSTAMALIGPPVVFLEPTTGMDPKARRFLWNCALSVVKEGRSVVLT	2040

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Qy      2041 SHSMEECEALCTRMALMVNGRFRCLGSGVQHLLKNRFGDGYTIVVRIAGSNPDLKPVQDFFG 2100
          |||
Db      2041 SHSMEECEALCTRMALMVNGRFRCLGSGVQHLLKNRFGDGYTIVVRIAGSNPDLKPVQEFFG 2100

Qy      2101 LAFFPGSVPEKHRNMLQYQLPSSLSSSLARIFSILSQSKRLHIEDYSVSQTTLDQVVFVN 2160
          |||
Db      2101 LAFFPGSVLKEKHRNMLQYQLPSSLSSSLARIFSILSQSKRLHIEDYSVSQTTLDQVVFVN 2160

Qy      2161 AKDQSDDDHLKDLKSLHKNQTVVDVAVLTSFLQDEKVKESYV 2201
          |||
Db      2161 AKDQSDDDHLKDLKSLHKNQTVVDVAVLTSFLQDEKVKESYV 2201

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SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	11466	100.0	2261	1	ABC1_HUMAN	O95477 homo sapien
2	10906	95.1	2261	1	ABC1_MOUSE	P41233 mus musculu
3	5689.5	49.6	2273	1	ABCR_HUMAN	P78363 homo sapien
4	4131	36.0	2436	1	ABC2_HUMAN	Q9bzc7 homo sapien
5	3989.5	34.8	2434	1	ABC2_MOUSE	P41234 mus musculu
6	2635.5	23.0	1704	1	ABC3_HUMAN	Q99758 homo sapien
7	1528.5	13.3	1704	1	CED7_CAEEL	P34358 caenorhabdi
8	411	3.6	330	1	DRRA_STRPE	P32010 streptomyce
9	380.5	3.3	343	1	NOD1_RHISN	P55476 rhizobium s
10	366	3.2	304	1	NOD1_RHIS3	P72335 rhizobium s
11	347	3.0	308	1	YADG_ECOLI	P36879 escherichia
12	347	3.0	335	1	NDI2_RHIME	Q8gnh6 rhizobium m
13	344.5	3.0	340	1	NOD1_RHILO	P23703 rhizobium l
14	343.5	3.0	347	1	NOD1_RHIGA	P50332 rhizobium g
15	335.5	2.9	1280	1	MDR1_HUMAN	P08183 homo sapien
16	331.5	2.9	355	1	NDI1_RHIME	O52618 rhizobium m
17	329.5	2.9	578	1	YBHF_ECOLI	P75776 escherichia
18	327	2.9	894	1	YHIH_ECOLI	P37624 escherichia
19	327	2.9	1276	1	MDR3_MOUSE	P21447 mus musculu

RESULT 2

ABC1_MOUSE

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ID  ABC1_MOUSE      STANDARD;      PRT;  2261 AA.
AC  P41233;
DT  01-FEB-1995 (Rel. 31, Created)
DT  16-OCT-2001 (Rel. 40, Last sequence update)
DT  15-SEP-2003 (Rel. 42, Last annotation update)
DE  ATP-binding cassette, sub-family A, member 1 (ATP-binding cassette
DE  transporter 1) (ATP-binding cassette 1) (ABC-1).
GN  ABCA1 OR ABC1.
OS  Mus musculus (Mouse).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX  NCBI_TaxID=10090;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=DBA/2; TISSUE=Macrophage;
RX  MEDLINE=94375008; PubMed=8088782;
RA  Luciani M.F., Denizot F., Savary S., Mattei M.-G., Chimini G.;
RT  "Cloning of two novel ABC transporters mapping on human chromosome
RT  9.";
RL  Genomics 21:150-159(1994).
RN  [2]
RP  SEQUENCE FROM N.A.
RC  STRAIN=C57BL/6J;
RX  MEDLINE=21251004; PubMed=11352567;
RA  Qiu Y., Cavellier L., Chiu S., Yang X., Rubin E., Cheng J.-F.;
RT  "Human and mouse ABCA1 comparative sequencing and transgenesis

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RT studies revealing novel regulatory sequences.";
RL Genomics 73:66-76(2001).
CC -!- FUNCTION: CAMP-DEPENDENT AND SULFONYLUREA-SENSITIVE ANION
CC TRANSPORTER. KEY GATEKEEPER INFLUENCING INTRACELLULAR CHOLESTEROL
CC TRANSPORT (BY SIMILARITY).
CC -!- TISSUE SPECIFICITY: WIDELY EXPRESSED IN ADULT TISSUES. HIGHEST
CC LEVELS ARE FOUND IN PREGNANT UTERUS AND UTERUS.
CC -!- DOMAIN: MULTIFUNCTIONAL POLYPEPTIDE WITH TWO HOMOLOGOUS HALVES,
CC EACH CONTAINING AN HYDROPHOBIC MEMBRANE-ANCHORING DOMAIN AND AN
CC ATP BINDING CASSETTE (ABC) DOMAIN.
CC -!- PTM: Phosphorylation on Ser-2054 regulates phospholipid efflux (By
CC similarity).
CC -!- SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY. ABCA SUBFAMILY.
CC -----
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DR EMBL; X75926; CAA53530.1; ALT_INIT.
DR EMBL; AF287263; AAG39073.1; ALT_INIT.
DR MGD; MGI:99607; Abcal.
DR GO; GO:0008203; P:cholesterol metabolism; IDA.
DR GO; GO:0030301; P:cholesterol transport; IDA.
DR InterPro; IPR003593; AAA_ATPase.
DR InterPro; IPR003439; ABC_transporter.
DR Pfam; PF00005; ABC_tran; 2.
DR ProDom; PD000006; ABC_transporter; 2.
DR SMART; SM00382; AAA; 2.
DR PROSITE; PS00211; ABC_TRANSPORTER_1; 1.
DR PROSITE; PS50893; ABC_TRANSPORTER_2; 2.
KW ATP-binding; Glycoprotein; Transmembrane; Transport; Phosphorylation.
FT TRANSMEM 26 42 POTENTIAL.
FT TRANSMEM 640 656 POTENTIAL.
FT TRANSMEM 690 706 POTENTIAL.
FT TRANSMEM 717 733 POTENTIAL.
FT TRANSMEM 749 765 POTENTIAL.
FT TRANSMEM 771 787 POTENTIAL.
FT TRANSMEM 1041 1057 POTENTIAL.
FT TRANSMEM 1351 1367 POTENTIAL.
FT TRANSMEM 1661 1677 POTENTIAL.
FT TRANSMEM 1708 1724 POTENTIAL.
FT TRANSMEM 1737 1753 POTENTIAL.
FT TRANSMEM 1775 1791 POTENTIAL.
FT TRANSMEM 1854 1870 POTENTIAL.
FT NP_BIND 933 940 ATP (POTENTIAL).
FT NP_BIND 1946 1953 ATP (POTENTIAL).
FT MOD_RES 1042 1042 PHOSPHORYLATION (BY PKA) (MAJOR) (BY
FT SIMILARITY).
FT MOD_RES 2054 2054 PHOSPHORYLATION (BY PKA) (MAJOR) (BY
FT SIMILARITY).
FT CARBOHYD 14 14 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 98 98 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 151 151 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 161 161 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 196 196 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 244 244 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 292 292 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 337 337 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 349 349 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 400 400 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 478 478 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 489 489 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 521 521 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 820 820 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1144 1144 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1294 1294 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1453 1453 N-LINKED (GLCNAC. . .) (POTENTIAL).

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FT	CARBOHYD	1499	1499	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	1504	1504	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	1637	1637	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	2044	2044	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	2238	2238	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CONFLICT	1567	1568	MISSING (IN REF. 2).
FT	CONFLICT	2024	2024	MISSING (IN REF. 2).
SQ	SEQUENCE	2261	AA; 254011 MW; FAE62B21FD1D09F9 CRC64;	

Query Match 95.1%; Score 10906; DB 1; Length 2261;
 Best Local Similarity 94.8%; Pred. No. 0;
 Matches 2087; Conservative 54; Mismatches 60; Indels 0; Gaps 0;

Qy	1	MPSAGTLPWVQGIICNANNPCFRYPPTGEAPGVVGNFNKSIVARLFS	60
Db	61	MPSAGTLPWVQGIICNANNPCFRYPPTGEAPGVVGNFNKSIVSRLFSDAQRLLYSQRDT	120
Qy	61	SMKDMRKVLRTLQQIKKSSSNLKLQDFLVDNETFSGFLYHNLSLPKSTVDKMLRADVILH	120
Db	121	SIKDMHKVLRMLRQIKHPNSNLKLQDFLVDNETFSGFLQHNLSPRSTVDSLQXNVGLQ	180
Qy	121	KVFLQGYQLHLTSLCNGSKSEEMIQLGDQEVSELCGLPREKLAARVLRNSMDILKPIL	180
Db	181	KVFLQGYQLHLASLCNGSKLEETIQLGDAEVSALCGLPRKKLDAARVLRNMDILKPVV	240
Qy	181	RTLNSTSPFPSKELAEATKTLHSLGTLAQELFSMRWSMDRQEVMTNVSSTSTQI	240
Db	241	TKLNSTSHLPTQHLAEATTVLLDSLGLAQELFSTKSWSDMRQEVMTNVSSTSTQI	300
Qy	241	YQAVSRIVCGHPEGGLKIKSLNWYEDNNYKALFGNGTEEDAETFYDNSTTPYCNDLMK	300
Db	301	YQAVSRIVCGHPEGGLKIKSLNWYEDNNYKALFGGNTEEDVDTFYDNSTTPYCNDLMK	360
Qy	301	NLESSPLSRIIWKALKPLLVGKILYTPDTPATRQVMAEVNKTQELAVFHDLEGMWEELS	360
Db	361	NLESSPLSRIIWKALKPLLVGKILYTPDTPATRQVMAEVNKTQELAVFHDLEGMWEELS	420
Qy	361	PKIWTFMENSQEMDLVRMLLDSRDNDHFWEQQLDGLDWTADQDIVAFLAKHPEDVQSSNGS	420
Db	421	PQIWTFMENSQEMDLVRTLLDSRGNDQFWEQKLDGLDWTADQDIMAFLAKNPEDVQSPNGS	480
Qy	421	VYTWREAFNETNQAIQTISRMECVNLNKLEPIATEVWLINKSMELDERKFWAGIVFTG	480
Db	481	VYTWREAFNETNQAIQTISRMECVNLNKLEPIPTVRLINKSMELDERKFWAGIVFTG	540
Qy	481	ITPGSIELPHHVYKIRMDIDNVERTNKIKDGYWDPGPRADPFEDMRYVWGGFAYLQDVV	540
Db	541	ITPDSVELPHHVYKIRMDIDNVERTNKIKDGYWDPGPRADPFEDMRYVWGGFAYLQDVV	600
Qy	541	EQAIIRVLTGTEKKTGVYVQMPYPCYVDDIFLRVMSRSMPLFMTLAWIYSVAVIIGIV	600
Db	601	EQAIIRVLTGSEKKTGVYVQMPYPCYVDDIFLRVMSRSMPLFMTLAWIYSVAVIISIV	660
Qy	601	YEKEARKETMRIMGLDNLWFSWFISSLIPLLVSAGLLVVILKGNLLPYSDPSVVFV	660
Db	661	YEKEARKETMRIMGLDNLWFSWVSSLIPLLVSAGLLVVILKGNLLPYSDPSVVFV	720
Qy	661	FLSVFAVVTILQCFLISTLFSRANLAAACGGIYFTLYLPYVLCVAWQDYVGFTLKIFAS	720
Db	721	FLSVFAMVTILQCFLISTLFSRANLAAACGGIYFTLYLPYVLCVAWQDYVGFSIKIFAS	780
Qy	721	LLSPVAFGFGCEYFALFEEQIGVQWDLNFESPVEEDGFNLTTSVSMMLFDTFLYGVMTW	780
Db	781	LLSPVAFGFGCEYFALFEEQIGVQWDLNFESPVEEDGFNLTTAVSMMLFDTFLYGVMTW	840
Qy	781	YIEAVFPQYGIIPRPWYFPCTKSYWFGESDEKSHPGSNQKRISIEICMEEPTHKLGVLS	840
Db	841	YIEAVFPQYGIIPRPWYFPCTKSYWFGEEIDEKSHPGSSQKGVSEICMEEPTHRLGVLS	900
Qy	841	IQLNVKVYRDGMKVAVDGLALNFYEGQITSFLGHNGAGKTTTMSILTGLFPPTSGTAYIL	900

Db 901 IQNLVKVYRDGMKVAVDGLALNFYEQITSFLGHNGAGKTTTMSILTGLFPPTSGTAYIL 960
 Qy 901 GKDIRSEMSTIRQNLGVCQHNVLFDMLTVEEHIWFYARLKLSEKHVKAEMEQLMADV 960
 Db 961 GKDIRSEMSSIRQNLGVCQHNVLFDMLTVEEHIWFYARLKLSEKHVKAEMEQLMADV 1020
 Qy 961 LPSSKLKSKTSQLSGGMQRKLSVALAFVGGSKVVILDEPTAGVDPYSRRGIWELLLKYRQ 1020
 Db 1021 LPSSKLKSKTSQLSGGMQRKLSVALAFVGGSKVVILDEPTAGVDPYSRRGIWELLLKYRQ 1080
 Qy 1021 GRTIILSTHHMDEADVLDRIAII SHGKLCCVGSFLKNQLGTGYLTLVKKDVESLS 1080
 Db 1081 GRTIILSTHHMDEADILGRIAII SHGKLCCVGSFLKNQLGTGYLTLVKKDVESLS 1140
 Qy 1081 SCRNSSSTVSYLKEDSVSQSSDAGLSDHESDTLTIDVSAISNLIRKHVSEARLVEDI 1140
 Db 1141 SCRNSSSTVSCLKEDSVSQSSDAGLSDHESDTLTIDVSAISNLIRKHVSEARLVEDI 1200
 Qy 1141 GHELTIVLPYEAAKEGAFVELFHEIDRLSDLGISYGISETTLEEIFLKVAEESGVDAE 1200
 Db 1201 GHELTIVLPYEAAKEGAFVELFHEIDRLSDLGISYGISETTLEEIFLKVAEESGVDAE 1260
 Qy 1201 TSDGTLPARNRRAFGDKQSCLPFTEDDAADPNDSIDPESRETDLGMDGKGSYQVK 1260
 Db 1261 TSDGTLPARNRRAFGDKQSCLPFTEDDAADPNDSIDPESRETDLGMDGKGSYQVK 1320
 Qy 1261 GWKLTQQQFVALLWKRLLIARRSRKGFQAIVLPAVFVCIALVFSLIVPPFGKYPSELEQ 1320
 Db 1321 GWKLTQQQFVALLWKRLLIARRSRKGFQAIVLPAVFVCIALVFSLIVPPFGKYPSELEQ 1380
 Qy 1321 PWMYNEQYTFVSNDAPEDTGTLELLNALTDPGFGTRCMEGNPIPDTPCQAGEEWTAP 1380
 Db 1381 PWMYNEQYTFVSNDAPEDMGTQELLNALTDPGFGTRCMEGNPIPDTPCLAGEEDWTISP 1440
 Qy 1381 VPQTIMDLFQNGNWTMKNPSPACQCSSDKIKMLPVCPPGAGGLPPPQRKQNTADIQLDL 1440
 Db 1441 VPQSIVDLFQNGNWTMKNPSPACQCSSDKIKMLPVCPPGAGGLPPPQRKQNTADIQLDL 1500
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 Db 1501 TGRNISDYLKTYVQIIAKSLKNIWNEFRYGGFSLGVSNTQALPPSQEVNDATKQMKK 1560
 Qy 1501 HLKLAKDSSADRFLNSLGRFMTGLDTRNNVKVWFNNKGWHAISSFLNINNAILRANLQK 1560
 Db 1561 HLKLAKDSSADRFLNSLGRFMTGLDTRNNVKVWFNNKGWHAISSFLNINNAILRANLQK 1620
 Qy 1561 GENPSHYGITAFNHPLNLTQQLSEVAPMTTSVDVLVSICVIFAMSFVPASFVFLIQR 1620
 Db 1621 GENPSHYGITAFNHPLNLTQQLSEVAPMTTSVDVLVSICVIFAMSFVPASFVFLIQR 1680
 Qy 1621 VSKAKHLQFISGVKPIYWLNSFVWDMCNYVVPATLVIIIFICFQKQSYVSSTNLPVAL 1680
 Db 1681 VSKAKHLQFISGVKPIYWLNSFVWDMCNYVVPATLVIIIFICFQKQSYVSSTNLPVAL 1740
 Qy 1681 LLLLYGWSITPLMYPASFVFKIPSTAYVVLTSVNLFIGINGSVATFVLELFTDNKLNNIN 1740
 Db 1741 LLLLYGWSITPLMYPASFVFKIPSTAYVVLTSVNLFIGINGSVATFVLELFTDNKLNNIN 1800
 Qy 1741 DILKSVFLIFPHFCLGRGLIDMVKNQAMADALERFGENRFVSPLSWDLVGRNLFAMAVEG 1800
 Db 1801 DILKSVFLIFPHFCLGRGLIDMVKNQAMADALERFGENRFVSPLSWDLVGRNLFAMAVEG 1860
 Qy 1801 VVFFLITVLIQYRFFIRPRPVNAKLSPLNDEDEDVRRERQRILDGGGQNDILEIKELTKI 1860
 Db 1861 VVFFLITVLIQYRFFIRPRPVNAKLSPLNDEDEDVRRERQRILDGGGQNDILEIKELTKI 1920
 Qy 1861 YRRKRKPAVDRICVIGIPPGECFLLGVNGAGKSTTFKMLTGDTTVTRGDAFLNRNSILSN 1920
 Db 1921 YRRKRKPAVDRICVIGIPPGECFLLGVNGAGKSTTFKMLTGDTTVTRGDAFLNRNSILSN 1980
 Qy 1921 IHEVHQNMGYCQPFDAITELLTGREHVEFFALLRGVPEKEVGKVGWAIKRLGLVKYGEK 1980

Db	1981	IHEVHQNMGYCPQFDAITELLTGREHVEFFALLRGVPEKEVGKFGEWAIRKLGKLVKYGEK	2040
Qy	1981	YAGNYSGGNKRKRLSTAMALIGGPPVVFLDEPTTGMDPKARRFLWNCALSVVKEGRSVVLT	2040
Db	2041	YASNYSGGNKRKRLSTAMALIGGPPVVFLDEPTTGMDPKARRFLWNCALSIVKEGRSVVLT	2100
Qy	2041	SHSMEECEALCTRMAIMVNGRFRCLGSVQHLKNRFGDGYTIVVRIAGSNPDLKPVQDFFG	2100
Db	2101	SHSMEECEALCTRMAIMVNGRFRCLGSVQHLKNRFGDGYTIVVRIAGSNPDLKPVQEFFG	2160
Qy	2101	LAFPGSVPEKHRNMLQYQLPSSLSSLARIFSILSQSKKRLHIEDYSVSQTTLDQVFNF	2160
Db	2161	LAFPGSVLKEKHRNMLQYQLPSSLSSLARIFSILSQSKKRLHIEDYSVSQTTLDQVFNF	2220
Qy	2161	AKDQSDDDHLKDLSLHKNQTVVDVAVLTSFLQDEKVKESYV	2201
Db	2221	AKDQSDDDHLKDLSLHKNQTVVDVAVLTSFLQDEKVKESYV	2261

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NEWS	4	Feb 24	TEMA now available on STN
NEWS	5	Feb 26	NTIS now allows simultaneous left and right truncation
NEWS	6	Feb 26	PCTFULL now contains images
NEWS	7	Mar 04	SDI PACKAGE for monthly delivery of multifile SDI results
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NEWS	9	Mar 24	Additional information for trade-named substances without structures available in REGISTRY
NEWS	10	Apr 11	Display formats in DGENE enhanced
NEWS	11	Apr 14	MEDLINE Reload
NEWS	12	Apr 17	Polymer searching in REGISTRY enhanced
NEWS	13	SEP 09	CA/CAPLUS records now contain indexing from 1907 to the present
NEWS	14	Apr 21	New current-awareness alert (SDI) frequency in WPIDS/WPINDEX/WPIX
NEWS	15	Apr 28	RDISCLOSURE now available on STN
NEWS	16	May 05	Pharmacokinetic information and systematic chemical names added to PHAR
NEWS	17	May 15	MEDLINE file segment of TOXCENTER reloaded
NEWS	18	May 15	Supporter information for ENCOMPAT and ENCOMPLIT updated
NEWS	19	May 19	Simultaneous left and right truncation added to WSCA
NEWS	20	May 19	RAPRA enhanced with new search field, simultaneous left and right truncation
NEWS	21	Jun 06	Simultaneous left and right truncation added to CBNB
NEWS	22	Jun 06	PASCAL enhanced with additional data
NEWS	23	Jun 20	2003 edition of the FSTA Thesaurus is now available
NEWS	24	Jun 25	HSDB has been reloaded
NEWS	25	Jul 16	Data from 1960-1976 added to RDISCLOSURE
NEWS	26	Jul 21	Identification of STN records implemented
NEWS	27	Jul 21	Polymer class term count added to REGISTRY
NEWS	28	Jul 22	INPADOC: Basic index (/BI) enhanced; Simultaneous Left and Right Truncation available
NEWS	29	AUG 05	New pricing for EUROPATFULL and PCTFULL effective August 1, 2003
NEWS	30	AUG 13	Field Availability (/FA) field enhanced in BEILSTEIN
NEWS	31	AUG 15	PATDPAFULL: one FREE connect hour, per account, in September 2003
NEWS	32	AUG 15	PCTGEN: one FREE connect hour, per account, in September 2003
NEWS	33	AUG 15	RDISCLOSURE: one FREE connect hour, per account, in September 2003
NEWS	34	AUG 15	TEMA: one FREE connect hour, per account, in September 2003
NEWS	35	AUG 18	Data available for download as a PDF in RDISCLOSURE
NEWS	36	AUG 18	Simultaneous left and right truncation added to PASCAL
NEWS	37	AUG 18	FROSTI and KOSMET enhanced with Simultaneous Left and Right

Truncation

NEWS 38 AUG 18 Simultaneous left and right truncation added to ANABSTR

NEWS EXPRESS April 4 CURRENT WINDOWS VERSION IS V6.01a, CURRENT
MACINTOSH VERSION IS V6.0b(ENG) AND V6.0Jb(JP),
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=> s schmitz gerd /au
L1 369 SCHMITZ GERD

=> s klucken jochen /au
L2 19 KLUCKEN JOCHEN

=> s atp (p) binding (p) cassette (p) gene
L3 3913 ATP (P) BINDING (P) CASSETTE (P) GENE

=> s abcal
L4 1030 ABCA1

=> s atp (s) binding (s) cassette (s) gene
L5 3077 ATP (S) BINDING (S) CASSETTE (S) GENE

=> s atp (s) binding (s) cassette (s) gene (s) protein
L6 2046 ATP (S) BINDING (S) CASSETTE (S) GENE (S) PROTEIN

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L2 ANSWER 1 OF 19 MEDLINE on STN

ACCESSION NUMBER: 2003356553 MEDLINE
 DOCUMENT NUMBER: 22745349 PubMed ID: 12861035
 TITLE: High efficacy of clonal growth and expansion of adult neural stem cells.
 AUTHOR: Wachs Frank-Peter; Couillard-Despres Sebastien; Engelhardt Maren; Wilhelm Daniel; Ploetz Sonja; Vroemen Maurice; Kaesbauer Johanna; Uyanik Goekhan; **Klucken Jochen**; Karl Claudia; Tebbing Johanna; Svendsen Clive; Weidner Norbert; Kuhn Hans-Georg; Winkler Juergen; Aigner Ludwig
 CORPORATE SOURCE: Volkswagen-Foundation Junior Group, University of Regensburg, Germany.
 SOURCE: LABORATORY INVESTIGATION, (2003 Jul) 83 (7) 949-62. Journal code: 0376617. ISSN: 0023-6837.
 PUB. COUNTRY: United States
 DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
 LANGUAGE: English
 FILE SEGMENT: Priority Journals
 ENTRY MONTH: 200308
 ENTRY DATE: Entered STN: 20030801
 Last Updated on STN: 20030813
 Entered Medline: 20030812

L2 ANSWER 2 OF 19 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC. on STN
 ACCESSION NUMBER: 2003:366865 BIOSIS
 DOCUMENT NUMBER: PREV200300366865
 TITLE: High efficacy of clonal growth and expansion of adult neural stem cells.
 AUTHOR(S): Wachs, Frank-Peter; Couillard-Despres, Sebastien; Engelhardt, Maren; Wilhelm, Daniel; Ploetz, Sonja; Vroemen, Maurice; Kaesbauer, Johanna; Uyanik, Goekhan; **Klucken, Jochen**; Karl, Claudia; Tebbing, Johanna; Svendsen, Clive; Weidner, Norbert; Kuhn, Hans-Georg; Winkler, Juergen; Aigner, Ludwig (1)
 CORPORATE SOURCE: (1) Department of Neurology, University of Regensburg, Franz-Josef-Strauss-Allee 11, D-93053, Regensburg, Germany: ludwig.aigner@klinik.uni-regensburg.de Germany
 SOURCE: Laboratory Investigation, (July 2003, 2003) Vol. 83, No. 7, pp. 949-962. print. ISSN: 0023-6837.
 DOCUMENT TYPE: Article
 LANGUAGE: English

L2 ANSWER 3 OF 19 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC. on STN
 ACCESSION NUMBER: 2001:64994 BIOSIS
 DOCUMENT NUMBER: PREV200100064994
 TITLE: Genomic organization and characterization of the promoter of the human ATP-binding cassette transporter-G1 (ABCG1) gene.
 AUTHOR(S): Langmann, Thomas; Porsch-Oezcueruemez, Mustafa; Unkelbach, Uwe; **Klucken, Jochen**; Schmitz, Gerd (1)
 CORPORATE SOURCE: (1) Institute for Clinical Chemistry and Laboratory Medicine, University of Regensburg, Franz-Josef-Strauss-Allee 11, 93042, Regensburg: gerd.schmitz@klinik.uni-regensburg.de Germany
 SOURCE: Biochimica et Biophysica Acta, (15 November, 2000) Vol. 1494, No. 1-2, pp. 175-180. print. ISSN: 0006-3002.
 DOCUMENT TYPE: Article
 LANGUAGE: English
 SUMMARY LANGUAGE: English

L2 ANSWER 4 OF 19 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC. on STN
 ACCESSION NUMBER: 2000:346957 BIOSIS
 DOCUMENT NUMBER: PREV200000346957

TITLE: Identification of a novel human sterol-sensitive
 ATP-binding cassette transporter (ABCA7).
 AUTHOR(S): Kaminski, Wolfgang E.; Orso, Evelyn; Diederich, Wendy;
 Klucken, Jochen; Drobnik, Wolfgang; Schmitz, Gerd
 (1)
 CORPORATE SOURCE: (1) Institute for Clinical Chemistry and Laboratory
 Medicine, University of Regensburg, Franz-Josef-Strauss-
 Allee 11, D-93042, Regensburg Germany
 SOURCE: Biochemical and Biophysical Research Communications, (July
 5, 2000) Vol. 273, No. 2, pp. 532-538. print.
 ISSN: 0006-291X.
 DOCUMENT TYPE: Article
 LANGUAGE: English
 SUMMARY LANGUAGE: English

L2 ANSWER 5 OF 19 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC. on STN
 ACCESSION NUMBER: 2000:113448 BIOSIS
 DOCUMENT NUMBER: PREV200000113448
 TITLE: ABCG1 (ABC8), the human homolog of the Drosophila white
 gene, is a regulator of macrophage cholesterol and
 phospholipid transport.
 AUTHOR(S): Klucken, Jochen; Buechler, Christa; Orso, Evelyn;
 Kaminski, Wolfgang E.; Porsch-Oezcueruemez, Mustafa;
 Liebisch, Gerhard; Kapinsky, Michael; Diederich, Wendy;
 Drobnik, Wolfgang; Dean, Michael; Allikmets, Rando;
 Schmitz, Gerd (1)
 CORPORATE SOURCE: (1) Institute for Clinical Chemistry and Laboratory
 Medicine, University of Regensburg, Franz-Josef-Strauss-
 Allee 11, D-93042, Regensburg Germany
 SOURCE: Proceedings of the National Academy of Sciences of the
 United States of America, (Jan. 18, 2000) Vol. 97, No. 2,
 pp. 817-822.
 ISSN: 0027-8424.
 DOCUMENT TYPE: Article
 LANGUAGE: English
 SUMMARY LANGUAGE: English

L2 ANSWER 6 OF 19 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC. on STN
 ACCESSION NUMBER: 2000:96559 BIOSIS
 DOCUMENT NUMBER: PREV200000096559
 TITLE: Regulation of scavenger receptor CD163 expression in human
 monocytes and macrophages by pro- and antiinflammatory
 stimuli.
 AUTHOR(S): Buechler, Christa; Ritter, Mirko; Orso, Evelyn; Langmann,
 Thomas; Klucken, Jochen; Schmitz, Gerd (1)
 CORPORATE SOURCE: (1) Institut fuer Klinische Chemie und
 Laboratoriumsmedizin, Klinikum der Universitaet Regensburg,
 Franz-Josef-Strauss-Allee 11, D-93042, Regensburg Germany
 SOURCE: Journal of Leukocyte Biology, (Jan., 2000) Vol. 67, No. 1,
 pp. 97-103.
 ISSN: 0741-5400.
 DOCUMENT TYPE: Article
 LANGUAGE: English
 SUMMARY LANGUAGE: English

L2 ANSWER 7 OF 19 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC. on STN
 ACCESSION NUMBER: 1999:386551 BIOSIS
 DOCUMENT NUMBER: PREV199900386551
 TITLE: The gene encoding ATP-binding cassette transporter 1 is
 mutated in Tangier disease.
 AUTHOR(S): Bodzioch, Marek; Orso, Evelyn; Klucken, Jochen;
 Langmann, Thomas; Boettcher, Alfred; Diederich, Wendy;
 Drobnik, Wolfgang; Barlage, Stefan; Buechler, Christa;
 Porsch-Oezcueruemez, Mustafa; Kaminski, Wolfgang E.;

Hahmann, Harry W.; Oette, Kurt; Rothe, Gregor; Aslanidis, Charalampos; Lackner, Karl J.; Schmitz, Gerd (1)

CORPORATE SOURCE: (1) Institute for Clinical Chemistry and Laboratory Medicine, University of Regensburg, D-93042, Regensburg Germany

SOURCE: Nature Genetics, (Aug., 1999) Vol. 22, No. 4, pp. 347-351. ISSN: 1061-4036.

DOCUMENT TYPE: Article

LANGUAGE: English

SUMMARY LANGUAGE: English

L2 ANSWER 8 OF 19 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC. on STN

ACCESSION NUMBER: 1999:247874 BIOSIS

DOCUMENT NUMBER: PREV199900247874

TITLE: Molecular cloning of the human ATP-binding cassette transporter 1 (hABC1): Evidence for sterol-dependent regulation in macrophages.

AUTHOR(S): Langmann, Thomas; **Klucken, Jochen**; Reil, Markus; Liebisch, Gerhard; Luciani, Marie-Francoise; Chimini, Giovanna; Kaminski, Wolfgang E.; Schmitz, Gerd (1)

CORPORATE SOURCE: (1) Institute for Clinical Chemistry and Laboratory Medicine, University of Regensburg, Franz-Josef-Strauss-Allee 11, D-93042, Regensburg Germany

SOURCE: Biochemical and Biophysical Research Communications, (April 2, 1999) Vol. 257, No. 1, pp. 29-33. ISSN: 0006-291X.

DOCUMENT TYPE: Article

LANGUAGE: English

SUMMARY LANGUAGE: English

L2 ANSWER 9 OF 19 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC. on STN

ACCESSION NUMBER: 1997:522758 BIOSIS

DOCUMENT NUMBER: PREV199799821961

TITLE: Scavenging, signalling and adhesion coupling in macrophages: Implications for atherogenesis.

AUTHOR(S): Schmitz, Gerd (1); Orso, Evelyn; Rothe, Gregor; **Klucken, Jochen**

CORPORATE SOURCE: (1) Inst. Clinical Chem. Lab. Med., Univ. Regensburg, Franz-Josef-Strauss-Allee 11, D-93053 Regensburg Germany

SOURCE: Current Opinion in Lipidology, (1997) Vol. 8, No. 5, pp. 287-300. ISSN: 0957-9672.

DOCUMENT TYPE: General Review

LANGUAGE: English

L2 ANSWER 10 OF 19 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC. on STN

ACCESSION NUMBER: 1997:61424 BIOSIS

DOCUMENT NUMBER: PREV199799360627

TITLE: Peripheral blood mononuclear phagocyte subpopulations as cellular markers in hypercholesterolemia.

AUTHOR(S): Rothe, Gregor; Gabriel, Holger; Kovacs, Eva; **Klucken, Jochen**; Stoehr, Josef; Kindermann, Wilfried; Schmitz, Gerd

CORPORATE SOURCE: Inst. Clinical Chemistry Lab. Med., Univ. Regensburg, Franz-Josef-Strauss-Allee 11, D-93053 Regensburg Germany

SOURCE: Arteriosclerosis Thrombosis and Vascular Biology, (1996) Vol. 16, No. 12, pp. 1437-1447. ISSN: 1079-5642.

DOCUMENT TYPE: Article

LANGUAGE: English

L2 ANSWER 11 OF 19 CAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 2001:9149 CAPLUS

DOCUMENT NUMBER: 135:1154

TITLE: Genomic organization and characterization of the promoter of the human ATP-binding cassette transporter-G1 (ABCG1) gene

AUTHOR(S): Langmann, Thomas; Porsch-Ozcurumez, Mustafa; Unkelbach, Uwe; Klucken, Jochen; Schmitz, Gerd

CORPORATE SOURCE: Institute for Clinical Chemistry and Laboratory Medicine, University of Regensburg, Regensburg, 93042, Germany

SOURCE: Biochimica et Biophysica Acta (2000), 1494(1-2), 175-180
CODEN: BBACAQ; ISSN: 0006-3002

PUBLISHER: Elsevier Science B.V.

DOCUMENT TYPE: Journal

LANGUAGE: English

REFERENCE COUNT: 26 THERE ARE 26 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L2 ANSWER 12 OF 19 CAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 2000:426543 CAPLUS

DOCUMENT NUMBER: 133:220696

TITLE: Identification of a Novel Human Sterol-Sensitive ATP-Binding Cassette Transporter (ABCA7)

AUTHOR(S): Kaminski, Wolfgang E.; Orso, Evelyn; Diederich, Wendy; Klucken, Jochen; Drobnik, Wolfgang; Schmitz, Gerd

CORPORATE SOURCE: Institute for Clinical Chemistry and Laboratory Medicine, University of Regensburg, Regensburg, D-93042, Germany

SOURCE: Biochemical and Biophysical Research Communications (2000), 273(2), 532-538
CODEN: BBRCA9; ISSN: 0006-291X

PUBLISHER: Academic Press

DOCUMENT TYPE: Journal

LANGUAGE: English

L2 ANSWER 13 OF 19 CAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 2000:227775 CAPLUS

DOCUMENT NUMBER: 132:275181

TITLE: ATP-binding cassette genes and proteins for diagnosis and treatment of lipid disorders and inflammatory diseases

INVENTOR(S): Schmitz, Gerd; Klucken, Jochen

PATENT ASSIGNEE(S): Bayer Aktiengesellschaft, Germany

SOURCE: PCT Int. Appl., 154 pp.
CODEN: PIXXD2

DOCUMENT TYPE: Patent

LANGUAGE: English

FAMILY ACC. NUM. COUNT: 1

PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2000018912	A2	20000406	WO 1999-EP6991	19990921
WO 2000018912	A3	20000817		
W:	AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CR, CU, CZ, DE, DK, DM, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM			
RW:	GH, GM, KE, LS, MW, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG			

CA 2344107	AA 20000406	CA 1999-2344107	19990921
AU 9959804	A1 20000417	AU 1999-59804	19990921
EP 1115865	A2 20010718	EP 1999-969740	19990921
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO			
JP 2002525111	T2 20020813	JP 2000-572359	19990921
PRIORITY APPLN. INFO.:		US 1998-101706P	P 19980925
		WO 1999-EP6991	W 19990921

L2 ANSWER 14 OF 19 CAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 2000:82248 CAPLUS

DOCUMENT NUMBER: 132:248860

TITLE: ABCG1 (ABC8), the human homolog of the Drosophila white gene, is a regulator of macrophage cholesterol and phospholipid transport

AUTHOR(S): Klucken, Jochen; Buchler, Christa; Orso, Evelyn; Kaminski, Wolfgang E.; Porsch-Ozcurumez, Mustafa; Liebisch, Gerhard; Kapinsky, Michael; Diederich, Wendy; Drobnik, Wolfgang; Dean, Michael; Allikmets, Rando; Schmitz, Gerd

CORPORATE SOURCE: Institute for Clinical Chemistry and Laboratory Medicine, University of Regensburg, Regensburg, 93042, Germany

SOURCE: Proceedings of the National Academy of Sciences of the United States of America (2000), 97(2), 817-822
CODEN: PNASA6; ISSN: 0027-8424

PUBLISHER: National Academy of Sciences

DOCUMENT TYPE: Journal

LANGUAGE: English

REFERENCE COUNT: 41 THERE ARE 41 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L2 ANSWER 15 OF 19 CAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 2000:62019 CAPLUS

DOCUMENT NUMBER: 132:206903

TITLE: Regulation of scavenger receptor CD163 expression in human monocytes and macrophages by pro- and antiinflammatory stimuli

AUTHOR(S): Buechler, Christa; Ritter, Mirko; Orso, Evelyn; Langmann, Thomas; Klucken, Jochen; Schmitz, Gerd

CORPORATE SOURCE: Institut fur Klinische Chemie und Laboratoriumsmedizin, Klinikum der Universitat Regensburg, Regensburg, D-93042, Germany

SOURCE: Journal of Leukocyte Biology (2000), 67(1), 97-103
CODEN: JLBIE7; ISSN: 0741-5400

PUBLISHER: Federation of American Societies for Experimental Biology

DOCUMENT TYPE: Journal

LANGUAGE: English

REFERENCE COUNT: 47 THERE ARE 47 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L2 ANSWER 16 OF 19 CAPLUS COPYRIGHT 2003 ACS on STN

ACCESSION NUMBER: 1999:500267 CAPLUS

DOCUMENT NUMBER: 131:255941

TITLE: The gene encoding ATP-binding cassette transporter 1 is mutated in Tangier disease

AUTHOR(S): Bodzioch, Marek; Orso, Evelyn; Klucken, Jochen; Langmann, Thomas; Bottcher, Alfred; Diederich, Wendy; Drobnik, Wolfgang; Barlage, Stefan; Buchler, Christa; Porsch-Ozcurumez, Mustafa; Kaminski, Wolfgang E.; Hahmann, Harry W.; Oette, Kurt; Rothe, Gregor; Aslanidis, Charalampos; Lackner, Karl J.; Schmitz,

CORPORATE SOURCE: Gerd
Institute for Clinical Chemistry and Laboratory
Medicine, University of Regensburg, Regensburg,
D-93042, Germany
SOURCE: Nature Genetics (1999), 22(4), 347-351
CODEN: NGENEC; ISSN: 1061-4036
PUBLISHER: Nature America
DOCUMENT TYPE: Journal
LANGUAGE: English
REFERENCE COUNT: 29 THERE ARE 29 CITED REFERENCES AVAILABLE FOR THIS
RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L2 ANSWER 17 OF 19 CAPLUS COPYRIGHT 2003 ACS on STN
ACCESSION NUMBER: 1999:199124 CAPLUS
DOCUMENT NUMBER: 131:83698
TITLE: Molecular cloning of the human ATP-binding cassette
transporter 1 (hABC1): evidence for sterol-dependent
regulation in macrophages
AUTHOR(S): Langmann, Thomas; Klucken, Jochen; Reil,
Markus; Liebisch, Gerhard; Luciani, Marie-Francoise;
Chimini, Giovanna; Kaminski, Wolfgang E.; Schmitz,
Gerd
CORPORATE SOURCE: Institute for Clinical Chemistry and Laboratory
Medicine, University of Regensburg, Regensburg, 93042,
Germany
SOURCE: Biochemical and Biophysical Research Communications
(1999), 257(1), 29-33
CODEN: BBRCA9; ISSN: 0006-291X
PUBLISHER: Academic Press
DOCUMENT TYPE: Journal
LANGUAGE: English
REFERENCE COUNT: 22 THERE ARE 22 CITED REFERENCES AVAILABLE FOR THIS
RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L2 ANSWER 18 OF 19 CAPLUS COPYRIGHT 2003 ACS on STN
ACCESSION NUMBER: 1997:675284 CAPLUS
DOCUMENT NUMBER: 127:344497
TITLE: Scavenging, signaling and adhesion coupling in
macrophages: implications for atherogenesis
AUTHOR(S): Schmitz, Gerd; Orso, Evelyn; Rothe, Gregor;
Klucken, Jochen
CORPORATE SOURCE: Institute for Clinical Chemistry and Laboratory
Medicine, University of Regensburg, Regensburg,
D-93053, Germany
SOURCE: Current Opinion in Lipidology (1997), 8(5), 287-300
CODEN: COPLEU; ISSN: 0957-9672
PUBLISHER: Rapid Science Publishers
DOCUMENT TYPE: Journal; General Review
LANGUAGE: English

L2 ANSWER 19 OF 19 CAPLUS COPYRIGHT 2003 ACS on STN
ACCESSION NUMBER: 1997:54357 CAPLUS
DOCUMENT NUMBER: 126:116448
TITLE: Peripheral blood mononuclear phagocyte subpopulations
as cellular markers in hypercholesterolemia
AUTHOR(S): Rothe, Gregor; Gabriel, Holger; Kovacs, Eva;
Klucken, Jochen; Stoehr, Josef; Kindermann,
Wilfried; Schmitz, Gerd
CORPORATE SOURCE: Inst. Clinical Chem. & Lab. Medicine, Univ.
Regensburg, Germany
SOURCE: Arteriosclerosis, Thrombosis, and Vascular Biology
(1996), 16(12), 1437-1447
CODEN: ATVBFA; ISSN: 1079-5642
PUBLISHER: American Heart Association

DOCUMENT TYPE:
LANGUAGE:

Journal
English